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```
Alignment No. 13362
     - gi No. 1542845
    - % Identity 83
     - Alignment Length 53
     - Location of Alignment 1n SEQ ID NO 1865: from 142 to 193
    - Alignment No. 13363
     - gi No. 2315514
     - % Identity 79.2
     - Alignment Length 144
     - Location of Alignment in SEQ ID NO 1865: from 51 to 193
    - Alignment No. 13364
     - gi No. 2996008
    - % Identity 80.4
    - Alignment Length 153
    - Location of Alignment in SEQ ID NO 1865: from 44 to 193
    - Alignment No. 13365
    - gi No. 338687
    - % Identity 81.2
    - Alignment Length 149
    - Location of Alignment in SEQ ID NO 1865: from 46 to 193
    - Alignment No. 13366
    - gi No. 3845214
    - % Identity 75.7
    - Alignment Length 144
    - Location of Alignment in SEQ ID NO 1865: from 51 to 193
    - Alignment No. 13367
    - gi No. 468605
    - % Identity 74.8
    - Alignment Length 147
    - Location of Alignment in SEQ ID NO 1865: from 48 to 193
    - Alignment No. 13368
    - gi No. 4759034
    - % Identity 81.9
    - Alignment Length 149
    - Location of Alignment in SEQ ID NO 1865: from 46 to 193
    - Alignment No. 13369
    - gi No. 549010
    - % Identity 91.4
    - Alignment Length 151
    - Location of Alignment in SEQ ID NO 1865: from 44 to 193
    - Alignment No. 13370
    - gi No. 549011
    - % Identity 81.9
    - Alignment Length 149
    - Location of Alignment in SEQ ID NO 1865: from 46 to 193
    - Alignment No. 13371
    - gi No. 626763
    - % Identity 74.8
    - Alignment Length 147
    - Location of Alignment in SEQ ID NO 1865: from 48 to 193
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- Pat. Appln. SEQ ID NO 1866
- Ceres seq_id 1501545
- Location of start within SEQ ID NO 1864: at 131 nt.
- (C) Nomination and Annotation of Domains within Predicted Polypeptide(s)
 - (D) Related Amino Acid Sequences
 - Alignment No. 13372
 - gi No. 1155261
 - % Identity 90.1
 - Alignment Length 151
 - Location of Alignment in SEQ ID NO 1866: from 1 to 150
 - Alignment No. 13373
 - gi No. 135054
 - % Identity 74.1
 - Alignment Length 147
 - Location of Alignment in SEQ ID NO 1866: from 5 to 150
 - Alignment No. 13374
 - gi No. 1542845
 - % Identity 83
 - Alignment Length 53
 - Location of Alignment in SEQ ID NO 1866: from 99 to 150
 - Alignment No. 13375
 - gi No. 2315514
 - % Identity 79.2
 - Alignment Length 144
 - Location of Alignment in SEQ ID NO 1866: from 8 to 150
 - Alignment No. 13376
 - gi No. 2996008
 - % Identity 80.4
 - Alignment Length 153
 - Location of Alignment in SEQ ID NO 1866: from 1 to 150 $\,$
 - Alignment No. 13377
 - gi No. 338687
 - % Identity 81.2
 - Alignment Length 149
 - Location of Alignment in SEQ ID NO 1866: from 3 to 150
 - Alignment No. 13378
 - gi No. 3845214
 - % Identity 75.7
 - Alignment Length 144
 - Location of Alignment in SEQ ID NO 1866: from 8 to 150
 - Alignment No. 13379
 - gi No. 468605
 - % Identity 74.8
 - Alignment Length 147
 - Location of Alignment in SEQ ID NO 1866: from 5 to 150
 - Alignment No. 13380
 - gi No. 4759034
 - % Identity 81.9
 - Alignment Length 149
 - Location of Alignment in SEQ ID NO 1866: from 3 to 150

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- Alignment No. 13381
- gi No. 549010
- % Identity 91.4
- Alignment Length 151
- Location of Alignment in SEQ ID NO 1866: from 1 to 150
- Alignment No. 13382
- qi No. 549011
- % Identity 81.9
- Alignment Length 149
- Location of Alignment in SEQ ID NO 1866: from 3 to 150
- Alignment No. 13383
- gi No. 626763
- % Identity 74.8
- Alignment Length 147
- Location of Alignment in SEQ ID NO 1866: from 5 to 150
- (B) Polypeptide Sequence
 - Pat. Appln. SEQ ID NO 1867
 - Ceres seq id 1501546
 - Location of start within SEQ ID NO 1864: at 227 nt.
- - (D) Related Amino Acid Sequences
 - Alignment No. 13384
 - gi No. 1155261
 - % Identity 90.1
 - Alignment Length 151
 - Location of Alignment in SEQ ID NO 1867: from 1 to 118
 - Alignment No. 13385
 - gi No. 135054
 - % Identity 74.1
 - Alignment Length 147
 - Location of Alignment in SEQ ID NO 1867: from 1 to 118
 - Alignment No. 13386
 - gi No. 1542845
 - % Identity 83
 - Alignment Length 53
 - Location of Alignment in SEQ ID NO 1867: from 67 to 118
 - Alignment No. 13387
 - gi No. 2315514
 - % Identity 79.2
 - Alignment Length 144
 - Location of Alignment in SEQ ID NO 1867: from 1 to 118
 - Alignment No. 13388
 - gi No. 2996008
 - % Identity 80.4
 - Alignment Length 153
 - Location of Alignment in SEQ ID NO 1867: from 1 to 118
 - Alignment No. 13389
 - gi No. 338687
 - % Identity 81.2
 - Alignment Length 149
 - Location of Alignment in SEQ ID NO 1867: from 1 to 118

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- Alignment No. 13390
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- gi No. 3845214
- % Identity 75.7
- Alignment Length 144
- Location of Alignment in SEQ ID NO 1867: from 1 to 118
- Alignment No. 13391
- gi No. 468605
- % Identity 74.8
- Alignment Length 147
- Location of Alignment in SEQ ID NO 1867: from 1 to 118
- Alignment No. 13392
- gi No. 4759034
- % Identity 81.9
- Alignment Length 149
- Location of Alignment in SEQ ID NO 1867: from 1 to 118
- Alignment No. 13393
- gi No. 549010
- % Identity 91.4
- Alignment Length 151
- Location of Alignment in SEQ ID NO 1867: from 1 to 118
- Alignment No. 13394
- gi No. 549011
- % Identity 81.9
- Alignment Length 149
- Location of Alignment in SEQ ID NO 1867: from 1 to 118
- Alignment No. 13395
- gi No. 626763
- % Identity 74.8
- Alignment Length 147
- Location of Alignment in SEQ ID NO 1867: from 1 to 118

- (A) Polynucleotide Sequence
 - Pat. Appln. SEQ ID NO 1868
 - Ceres seq_id 1501547
 - (B) Polypeptide Sequence
 - Pat. Appln. SEQ ID NO 1869
 - Ceres seq_id 1501548
 - Location of start within SEQ ID NO 1868: at 2 nt.
- - Alignment No. 13396
 - Nucleoside diphosphate kinases
 - Location within SEQ ID NO 1869: from 94 to 241 aa.
 - (D) Related Amino Acid Sequences
 - Alignment No. 13397
 - gi No. 1076713
 - % Identity 87.5
 - Alignment Length 24
 - Location of Alignment in SEQ ID NO 1869: from 91 to 114
 - Alignment No. 13398
 - qi No. 1304478

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- % Identity 70
- Alignment Length 40
- Location of Alignment in SEQ ID NO 1869: from 91 to 130
- Alignment No. 13399
- gi No. 1729427
- % Identity 70
- Alignment Length 40
- Location of Alignment in SEQ ID NO 1869: from 91 to 130
- Alignment No. 13400
- gi No. 2129487
- % Identity 81
- Alignment Length 153
- Location of Alignment in SEQ ID NO 1869: from 91 to 243
- Alignment No. 13401
- gi No. 2829275
- % Identity 71.2
- Alignment Length 230
- Location of Alignment in SEQ ID NO 1869: from 15 to 243
- Alignment No. 13402
- gi No. 4972094
- % Identity 72.5
- Alignment Length 229
- Location of Alignment in SEQ ID NO 1869: from 15 to 243
- (B) Polypeptide Sequence
 - Pat. Appln. SEQ ID NO 1870
 - Ceres seq_id 1501549
 - Location of start within SEQ ID NO 1868: at 17 nt.
- (C) Nomination and Annotation of Domains within Predicted Polypeptide(s)
 - Alignment No. 13403
 - Nucleoside diphosphate kinases
 - Location within SEQ ID NO 1870: from 89 to 236 aa.
 - (D) Related Amino Acid Sequences
 - Alignment No. 13404
 - gi No. 1076713
 - % Identity 87.5
 - Alignment Length 24
 - Location of Alignment in SEQ ID NO 1870: from 86 to 109
 - Alignment No. 13405
 - gi No. 1304478
 - % Identity 70
 - Alignment Length 40
 - Location of Alignment in SEQ ID NO 1870: from 86 to 125
 - Alignment No. 13406
 - gi No. 1729427
 - % Identity 70
 - Alignment Length 40
 - Location of Alignment in SEQ ID NO 1870: from 86 to 125
 - Alignment No. 13407
 - gi No. 2129487
 - % Identity 81

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- Alignment Length 153
- Location of Alignment in SEQ ID NO 1870: from 86 to 238
- Alignment No. 13408
- gi No. 2829275
- % Identity 71.2
- Alignment Length 230
- Location of Alignment in SEQ ID NO 1870: from 10 to 238
- Alignment No. 13409
- gi No. 4972094
- % Identity 72.5
- Alignment Length 229
- Location of Alignment in SEQ ID NO 1870: from 10 to 238
- (B) Polypeptide Sequence
 - Pat. Appln. SEQ ID NO 1871
 - Ceres seq_id 1501550
 - Location of start within SEQ ID NO 1868: at 245 nt.
- - Alignment No. 13410
 - Nucleoside diphosphate kinases
 - Location within SEQ ID NO 1871: from 13 to 160 aa.
 - (D) Related Amino Acid Sequences
 - Alignment No. 13411
 - gi No. 1076713
 - % Identity 87.5
 - Alignment Length 24
 - Location of Alignment in SEQ ID NO 1871: from 10 to 33
 - Alignment No. 13412
 - gi No. 1304478
 - % Identity 70
 - Alignment Length 40
 - Location of Alignment in SEQ ID NO 1871: from 10 to 49
 - Alignment No. 13413
 - gi No. 1729427
 - % Identity 70
 - Alignment Length 40
 - Location of Alignment in SEQ ID NO 1871: from 10 to 49
 - Alignment No. 13414
 - gi No. 2129487
 - % Identity 81
 - Alignment Length 153
 - Location of Alignment in SEQ ID NO 1871: from 10 to 162
 - Alignment No. 13415
 - gi No. 2829275
 - % Identity 71.2
 - Alignment Length 230
 - Location of Alignment in SEQ ID NO 1871: from 1 to 162
 - Alignment No. 13416
 - qi No. 4972094
 - % Identity 72.5
 - Alignment Length 229

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- Location of Alignment in SEQ ID NO 1871: from 1 to 162

- (A) Polynucleotide Sequence
 - Pat. Appln. SEQ ID NO 1872
 - Ceres seq id 1501565
 - (B) Polypeptide Sequence
 - Pat. Appln. SEQ ID NO 1873
 - Ceres seq_id 1501566
 - Location of start within SEQ ID NO 1872: at 457 nt.
- - (D) Related Amino Acid Sequences
 - Alignment No. 13417
 - gi No. 1002689
 - % Identity 72
 - Alignment Length 25
 - Location of Alignment in SEQ ID NO 1873: from 7 to 31
 - Alignment No. 13418
 - gi No. 1172600
 - % Identity 82.9
 - Alignment Length 35
 - Location of Alignment in SEQ ID NO 1873: from 1 to 34
 - Alignment No. 13419
 - gi No. 130847
 - % Identity 78.8
 - Alignment Length 33
 - Location of Alignment in SEQ ID NO 1873: from 1 to 33
 - Alignment No. 13420
 - gi No. 130860
 - % Identity 88.2
 - Alignment Length 34
 - Location of Alignment in SEQ ID NO 1873: from 1 to 34
 - Alignment No. 13421
 - gi No. 2621771
 - % Identity 72
 - Alignment Length 25
 - Location of Alignment in SEQ ID NO 1873: from 7 to 31
 - Alignment No. 13422
 - qi No. 2650136
 - % Identity 72
 - Alignment Length 25
 - Location of Alignment in SEQ ID NO 1873: from 7 to 31
 - Alignment No. 13423
 - gi No. 3080509
 - % Identity 73.5
 - Alignment Length 34
 - Location of Alignment in SEQ ID NO 1873: from 1 to 34
 - Alignment No. 13424
 - gi No. 3114275
 - % Identity 79.3
 - Alignment Length 29
 - Location of Alignment in SEQ ID NO 1873: from 5 to 33

- Alignment No. 13425

- gi No. 3421096
- % Identity 94.3
- Alignment Length 35
- Location of Alignment in SEQ ID NO 1873: from 1 to 34
- Alignment No. 13426
- gi No. 3914413
- % Identity 93.9
- Alignment Length 33
- Location of Alignment in SEQ ID NO 1873: from 3 to 34
- Alignment No. 13427
- gi No. 3914424
- % Identity 91.4
- Alignment Length 35
- Location of Alignment in SEQ ID NO 1873: from 1 to 34
- Alignment No. 13428
- gi No. 3914431
- % Identity 94.3
- Alignment Length 35
- Location of Alignment in SEQ ID NO 1873: from 1 to 34
- Alignment No. 13429
- gi No. 3914438
- % Identity 88.2
- Alignment Length 34
- Location of Alignment in SEQ ID NO 1873: from 1 to 34
- Alignment No. 13430
- gi No. 3914440
- % Identity 71.4
- Alignment Length 35
- Location of Alignment in SEQ ID NO 1873: from 1 to 34
- Alignment No. 13431
- gi No. 4506183
- % Identity 88.2
- Alignment Length 34
- Location of Alignment in SEQ ID NO 1873: from 1 to 34
- Alignment No. 13432
- gi No. 542655
- % Identity 88.2
- Alignment Length 34
- Location of Alignment in SEQ ID NO 1873: from 1 to 34
- Alignment No. 13433
- gi No. 585729
- % Identity 70.8
- Alignment Length 24
- Location of Alignment in SEQ ID NO 1873: from 8 to 31

- (A) Polynucleotide Sequence
 - Pat. Appln. SEQ ID NO 1874
 - Ceres seq_id 1501567
 - (B) Polypeptide Sequence
 - Pat. Appln. SEQ ID NO 1875

- Ceres seq_id 1501568
- Location of start within SEQ ID NO 1874: at 46 nt.
- (C) Nomination and Annotation of Domains within Predicted Polypeptide(s)
 - (D) Related Amino Acid Sequences
 - (B) Polypeptide Sequence
 - Pat. Appln. SEQ ID NO 1876
 - Ceres seq id 1501569
 - Location of start within SEQ ID NO 1874: at 176 nt.
- - Alignment No. 13434
 - Ribosomal protein S11
 - Location within SEQ ID NO 1876: from 29 to 129 aa.
 - (D) Related Amino Acid Sequences
 - Alignment No. 13435
 - gi No. 1173200
 - % Identity 95.3
 - Alignment Length 64
 - Location of Alignment in SEQ ID NO 1876: from 67 to 129
 - Alignment No. 13436
 - gi No. 1173201
 - % Identity 86.5
 - Alignment Length 126
 - Location of Alignment in SEQ ID NO 1876: from 5 to 129
 - Alignment No. 13437
 - gi No. 131772
 - % Identity 96.9
 - Alignment Length 130
 - Location of Alignment in SEQ ID NO 1876: from 1 to 129
 - Alignment No. 13438
 - gi No. 131773
 - % Identity 94.5
 - Alignment Length 128
 - Location of Alignment in SEQ ID NO 1876: from 3 to 129
 - Alignment No. 13439
 - gi No. 133771
 - % Identity 81.7
 - Alignment Length 131
 - Location of Alignment in SEQ ID NO 1876: from 1 to 129
 - Alignment No. 13440
 - gi No. 133777
 - % Identity 78.2
 - Alignment Length 110
 - Location of Alignment in SEQ ID NO 1876: from 21 to 129
 - Alignment No. 13441
 - gi No. 133782
 - % Identity 78.8
 - Alignment Length 132
 - Location of Alignment in SEQ ID NO 1876: from 1 to 129

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- Alignment No. 13442
- gi No. 133785
- % Identity 84
- Alignment Length 131
- Location of Alignment in SEQ ID NO 1876: from 1 to 129
- Alignment No. 13443
- gi No. 133789
- % Identity 70.2
- Alignment Length 121
- Location of Alignment in SEQ ID NO 1876: from 10 to 129
- Alignment No. 13444
- gi No. 1346941
- % Identity 76.4
- Alignment Length 110
- Location of Alignment in SEQ ID NO 1876: from 21 to 129
- Alignment No. 13445
- gi No. 1350935
- % Identity 78.8
- Alignment Length 132
- Location of Alignment in SEQ ID NO 1876: from 1 to 129
- Alignment No. 13446
- gi No. 1350937
- % Identity 77.9
- Alignment Length 131
- Location of Alignment in SEQ ID NO 1876: from 1 to 129
- Alignment No. 13447
- gi No. 2350992
- % Identity 76
- Alignment Length 104
- Location of Alignment in SEQ ID NO 1876: from 27 to 129
- Alignment No. 13448
- gi No. 2414647
- % Identity 80.9
- Alignment Length 115
- Location of Alignment in SEQ ID NO 1876: from 16 to 129
- Alignment No. 13449
- gi No. 2500443
- % Identity 97.8
- Alignment Length 46
- Location of Alignment in SEQ ID NO 1876: from 85 to 129
- Alignment No. 13450
- gi No. 3097244
- % Identity 85.5
- Alignment Length 131
- Location of Alignment in SEQ ID NO 1876: from 1 to 129
- Alignment No. 13451
- gi No. 3122785
- % Identity 90
- Alignment Length 130
- Location of Alignment in SEQ ID NO 1876: from 1 to 129
- Alignment No. 13452

- gi No. 4574240
 % Identity 84.5
- Alignment Length 110
- Location of Alignment in SEQ ID NO 1876: from 21 to 129
- Alignment No. 13453
- gi No. 4588920
- % Identity 81.7
- Alignment Length 131
- Location of Alignment in SEQ ID NO 1876: from 1 to 129
- Alignment No. 13454
- gi No. 4678226
- % Identity 90.8
- Alignment Length 130
- Location of Alignment in SEQ ID NO 1876: from 1 to 129
- Alignment No. 13455
- gi No. 4886269
- % Identity 91.5
- Alignment Length 130
- Location of Alignment in SEQ ID NO 1876: from 1 to 129
- Alignment No. 13456
- gi No. 5032051
- % Identity 84.7
- Alignment Length 131
- Location of Alignment in SEQ ID NO 1876: from 1 to 129
- Alignment No. 13457
- qi No. 5441523
- % Identity 98.3
- Alignment Length 59
- Location of Alignment in SEQ ID NO 1876: from 72 to 129
- Alignment No. 13458
- gi No. 547604
- % Identity 77.3
- Alignment Length 110
- Location of Alignment in SEQ ID NO 1876: from 21 to 129
- Alignment No. 13459
- gi No. 70946
- % Identity 76.4
- Alignment Length 110
- Location of Alignment in SEQ ID NO 1876: from 21 to 129
- Alignment No. 13460
- gi No. 730453
- % Identity 77.3
- Alignment Length 110
- Location of Alignment in SEQ ID NO 1876: from 21 to 129
- Alignment No. 13461
- gi No. 730633
- % Identity 82.4
- Alignment Length 131
- Location of Alignment in SEQ ID NO 1876: from 1 to 129
- Alignment No. 13462
- gi No. 83794

- % Identity 80
- Alignment Length 130
- Location of Alignment in SEQ ID NO 1876: from 1 to 129
- (B) Polypeptide Sequence
 - Pat. Appln. SEQ ID NO 1877
 - Ceres seq_id 1501570
 - Location of start within SEQ ID NO 1874: at 350 nt.
- - Alignment No. 13463
 - Ribosomal protein S11
 - Location within SEQ ID NO 1877: from 1 to 71 aa.
 - (D) Related Amino Acid Sequences
 - Alignment No. 13464
 - gi No. 1173200
 - % Identity 95.3
 - Alignment Length 64
 - Location of Alignment in SEQ ID NO 1877: from 9 to 71
 - Alignment No. 13465
 - gi No. 1173201
 - % Identity 86.5
 - Alignment Length 126
 - Location of Alignment in SEQ ID NO 1877: from 1 to 71
 - Alignment No. 13466
 - gi No. 131772
 - % Identity 96.9
 - Alignment Length 130
 - Location of Alignment in SEQ ID NO 1877: from 1 to 71
 - Alignment No. 13467
 - gi No. 131773
 - % Identity 94.5
 - Alignment Length 128
 - Location of Alignment in SEQ ID NO 1877: from 1 to 71
 - Alignment No. 13468
 - gi No. 133771
 - % Identity 81.7
 - Alignment Length 131
 - Location of Alignment in SEQ ID NO 1877: from 1 to 71 $\,$
 - Alignment No. 13469
 - gi No. 133777
 - % Identity 78.2
 - Alignment Length 110
 - Location of Alignment in SEQ ID NO 1877: from 1 to 71
 - Alignment No. 13470
 - gi No. 133782
 - % Identity 78.8
 - Alignment Length 132
 - Location of Alignment in SEQ ID NO 1877: from 1 to 71
 - Alignment No. 13471
 - gi No. 133785
 - % Identity 84

- Alignment Length 131
- Location of Alignment in SEQ ID NO 1877: from 1 to 71
- Alignment No. 13472
- gi No. 133789
- % Identity 70.2
- Alignment Length 121
- Location of Alignment in SEQ ID NO 1877: from 1 to 71
- Alignment No. 13473
- gi No. 1346941
- % Identity 76.4
- Alignment Length 110
- Location of Alignment in SEQ ID NO 1877: from 1 to 71
- Alignment No. 13474
- gi No. 1350935
- % Identity 78.8
- Alignment Length 132
- Location of Alignment in SEQ ID NO 1877: from 1 to 71
- Alignment No. 13475
- gi No. 1350937
- % Identity 77.9
- Alignment Length 131
- Location of Alignment in SEQ ID NO 1877: from 1 to 71
- Alignment No. 13476
- gi No. 2350992
- % Identity 76
- Alignment Length 104
- Location of Alignment in SEQ ID NO 1877: from 1 to 71
- Alignment No. 13477
- gi No. 2414647
- % Identity 80.9
- Alignment Length 115
- Location of Alignment in SEQ ID NO 1877: from 1 to 71 $\,$
- Alignment No. 13478
- gi No. 2500443
- % Identity 97.8
- Alignment Length 46
- Location of Alignment in SEQ ID NO 1877: from 27 to 71 $\,$
- Alignment No. 13479
- gi No. 3097244
- % Identity 85.5
- Alignment Length 131
- Location of Alignment in SEQ ID NO 1877: from 1 to 71
- Alignment No. 13480
- gi No. 3122785
- % Identity 90
- Alignment Length 130
- Location of Alignment in SEQ ID NO 1877: from 1 to 71
- Alignment No. 13481
- gi No. 4574240
- % Identity 84.5
- Alignment Length 110

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- Location of Alignment in SEQ ID NO 1877: from 1 to 71
- Alignment No. 13482
- gi No. 4588920
- % Identity 81.7
- Alignment Length 131
- Location of Alignment in SEQ ID NO 1877: from 1 to 71
- Alignment No. 13483
- gi No. 4678226
- % Identity 90.8
- Alignment Length 130
- Location of Alignment in SEQ ID NO 1877: from 1 to 71
- Alignment No. 13484
- gi No. 4886269
- % Identity 91.5
- Alignment Length 130
- Location of Alignment in SEQ ID NO 1877: from 1 to 71
- Alignment No. 13485
- gi No. 5032051
- % Identity 84.7
- Alignment Length 131
- Location of Alignment in SEQ ID NO 1877: from 1 to 71
- Alignment No. 13486
- gi No. 5441523
- % Identity 98.3
- Alignment Length 59
- Location of Alignment in SEQ ID NO 1877: from 14 to 71
- Alignment No. 13487
- qi No. 547604
- % Identity 77.3
- Alignment Length 110
- Location of Alignment in SEQ ID NO 1877: from 1 to 71
- Alignment No. 13488
- gi No. 70946
- % Identity 76.4
- Alignment Length 110
- Location of Alignment in SEQ ID NO 1877: from 1 to 71
- Alignment No. 13489
- gi No. 730453
- % Identity 77.3
- Alignment Length 110
- Location of Alignment in SEQ ID NO 1877: from 1 to 71
- Alignment No. 13490
- gi No. 730633
- % Identity 82.4
- Alignment Length 131
- Location of Alignment in SEQ ID NO 1877: from 1 to 71
- Alignment No. 13491
- gi No. 83794
- % Identity 80
- Alignment Length 130
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- Location of Alignment in SEQ ID NO 1877: from 1 to 71

- (A) Polynucleotide Sequence
 - Pat. Appln. SEQ ID NO 1878
 - Ceres seq id 1501571
 - (B) Polypeptide Sequence
 - Pat. Appln. SEQ ID NO 1879
 - Ceres seq id 1501572
 - Location of start within SEQ ID NO 1878: at 1 nt.
- - (D) Related Amino Acid Sequences
 - Alignment No. 13492
 - gi No. 4506093
 - % Identity 72.7
 - Alignment Length 11
 - Location of Alignment in SEQ ID NO 1879: from 27 to 37 $\,$
 - Alignment No. 13493
 - gi No. 973307
 - % Identity 72.7
 - Alignment Length 11
 - Location of Alignment in SEQ ID NO 1879: from 27 to 37
 - (B) Polypeptide Sequence
 - Pat. Appln. SEQ ID NO 1880
 - Ceres seq_id 1501573
 - Location of start within SEQ ID NO 1878: at 2 nt.
- (C) Nomination and Annotation of Domains within Predicted Polypeptide(s) $% \left(\frac{1}{2}\right) =\frac{1}{2}\left(\frac{1}{2}\right) +\frac{1}{2}\left(\frac{1}{2}\right) +\frac{$
 - (D) Related Amino Acid Sequences
 - Alignment No. 13494
 - gi No. 2493240
 - % Identity 75
 - Alignment Length 16
 - Location of Alignment in SEQ ID NO 1880: from 145 to 158
 - Alignment No. 13495
 - gi No. 4808162
 - % Identity 76.9
 - Alignment Length 13
 - Location of Alignment in SEQ ID NO 1880: from 145 to 157
 - Alignment No. 13496
 - gi No. 4808164
 - % Identity 76.9
 - Alignment Length 13
 - Location of Alignment in SEQ ID NO 1880: from 145 to 157
 - Alignment No. 13497
 - gi No. 4808166
 - % Identity 76.9
 - Alignment Length 13
 - Location of Alignment in SEQ ID NO 1880: from 145 to 157
 - Alignment No. 13498
 - gi No. 4808177
 - % Identity 76.9
 - Alignment Length 13

- Location of Alignment in SEQ ID NO 1880: from 145 to 157
- (B) Polypeptide Sequence
 - Pat. Appln. SEQ ID NO 1881
 - Ceres seq id 1501574
 - Location of start within SEQ ID NO 1878: at 125 nt.
- - (D) Related Amino Acid Sequences
 - Alignment No. 13499
 - gi No. 2493240
 - % Identity 75
 - Alignment Length 16
 - Location of Alignment in SEQ ID NO 1881: from 104 to 117
 - Alignment No. 13500
 - gi No. 4808162
 - % Identity 76.9
 - Alignment Length 13
 - Location of Alignment in SEQ ID NO 1881: from 104 to 116
 - Alignment No. 13501
 - gi No. 4808164
 - % Identity 76.9
 - Alignment Length 13
 - Location of Alignment in SEQ ID NO 1881: from 104 to 116
 - Alignment No. 13502
 - gi No. 4808166
 - % Identity 76.9
 - Alignment Length 13
 - Location of Alignment in SEQ ID NO 1881: from 104 to 116 $\,$
 - Alignment No. 13503
 - gi No. 4808177
 - % Identity 76.9
 - Alignment Length 13
 - Location of Alignment in SEQ ID NO 1881: from 104 to 116

- (A) Polynucleotide Sequence
 - Pat. Appln. SEQ ID NO 1882
 - Ceres seq_id 1501582
 - (B) Polypeptide Sequence
 - Pat. Appln. SEQ ID NO 1883
 - Ceres seq_id 1501583
 - Location of start within SEQ ID NO 1882: at 268 nt.
- - (D) Related Amino Acid Sequences
 - Alignment No. 13504
 - gi No. 2655291
 - % Identity 84.4
 - Alignment Length 77
 - Location of Alignment in SEQ ID NO 1883: from 1 to 76
 - (B) Polypeptide Sequence
 - Pat. Appln. SEQ ID NO 1884
 - Ceres seq_id 1501584

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- Location of start within SEO ID NO 1882: at 352 nt.
- (C) Nomination and Annotation of Domains within Predicted Polypeptide(s)
 - (D) Related Amino Acid Sequences
 - Alignment No. 13505
 - gi No. 2655291
 - % Identity 84.4
 - Alignment Length 77
 - Location of Alignment in SEQ ID NO 1884: from 1 to 48

Maximum Length Sequence corresponding to clone ID 286175

- (A) Polynucleotide Sequence
 - Pat. Appln. SEQ ID NO 1885
 - Ceres seq_id 1501589
 - (B) Polypeptide Sequence
 - Pat. Appln. SEQ ID NO 1886
 - Ceres seq_id 1501590
 - Location of start within SEQ ID NO 1885: at 1 nt.
- - (D) Related Amino Acid Sequences
 - (B) Polypeptide Sequence
 - Pat. Appln. SEQ ID NO 1887
 - Ceres seg id 1501591
 - Location of start within SEQ ID NO 1885: at 3 nt.
- (C) Nomination and Annotation of Domains within Predicted Polypeptide(s) $\label{eq:polypeptide}$
 - Alignment No. 13506
 - Lysyl oxidase
 - Location within SEQ ID NO 1887: from 53 to 170 aa.
 - (D) Related Amino Acid Sequences
 - (B) Polypeptide Sequence
 - Pat. Appln. SEQ ID NO 1888
 - Ceres seq_id 1501592
 - Location of start within SEQ ID NO 1885: at 108 nt.
- - Alignment No. 13507
 - Lysyl oxidase
 - Location within SEQ ID NO 1888: from 18 to 135 aa.
 - (D) Related Amino Acid Sequences

- (A) Polynucleotide Sequence
 - Pat. Appln. SEQ ID NO 1889
 - Ceres seq_id 1501609
 - (B) Polypeptide Sequence
 - Pat. Appln. SEQ ID NO 1890
 - Ceres seq_id 1501610
 - Location of start within SEQ ID NO 1889: at 2 nt.
- (C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- (D) Related Amino Acid Sequences
- (B) Polypeptide Sequence
 - Pat. Appln. SEQ ID NO 1891
 - Ceres seq_id 1501611
 - Location of start within SEQ ID NO 1889: at 26 nt.
- (C) Nomination and Annotation of Domains within Predicted Polypeptide(s)
 - (D) Related Amino Acid Sequences
 - (B) Polypeptide Sequence
 - Pat. Appln. SEQ ID NO 1892
 - Ceres seq_id 1501612
 - Location of start within SEQ ID NO 1889: at 324 nt.
- (C) Nomination and Annotation of Domains within Predicted Polypeptide(s) $% \left(\frac{1}{2}\right) =\frac{1}{2}\left(\frac{1}{2}\right) +\frac{1}{2}\left(\frac{1}{2}\right) +\frac{$
 - Alignment No. 13508
 - Glycosyl hydrolase family 9
 - Location within SEQ ID NO 1892: from 3 to 42 aa.
 - (D) Related Amino Acid Sequences
 - Alignment No. 13509
 - gi No. 2765531
 - % Identity 76.7
 - Alignment Length 30
 - Location of Alignment in SEQ ID NO 1892: from 1 to 15

- (A) Polynucleotide Sequence
 - Pat. Appln. SEQ ID NO 1893
 - Ceres seq_id 1501624
 - (B) Polypeptide Sequence
 - Pat. Appln. SEQ ID NO 1894
 - Ceres seq_id 1501625
 - Location of start within SEQ ID NO 1893: at 1 nt.
- - (D) Related Amino Acid Sequences
 - Alignment No. 13510
 - gi No. 2135765
 - % Identity 75
 - Alignment Length 12
 - Location of Alignment in SEQ ID NO 1894: from 53 to 64
 - Alignment No. 13511
 - gi No. 4505285
 - % Identity 75
 - Alignment Length 12
 - Location of Alignment in SEQ ID NO 1894: from 53 to 64
 - Alignment No. 13512
 - gi No. 542994
 - % Identity 71.4
 - Alignment Length 14
 - Location of Alignment in SEQ ID NO 1894: from 21 to 34
 - (B) Polypeptide Sequence
 - Pat. Appln. SEQ ID NO 1895

- Ceres seq id 1501626
- Location of start within SEQ ID NO 1893: at 3 nt.
- (C) Nomination and Annotation of Domains within Predicted Polypeptide(s) $\label{eq:condition} % \begin{array}{c} \text{Polyperiod} \\ \text{Poly$
 - (D) Related Amino Acid Sequences
 - Alignment No. 13513
 - gi No. 2224619
 - % Identity 72.7
 - Alignment Length 11
 - Location of Alignment in SEQ ID NO 1895: from 58 to 68
 - Alignment No. 13514
 - gi No. 418612
 - % Identity 75
 - Alignment Length 12
 - Location of Alignment in SEQ ID NO 1895: from 57 to 68
 - (B) Polypeptide Sequence
 - Pat. Appln. SEQ ID NO 1896
 - Ceres seq id 1501627
 - Location of start within SEQ ID NO 1893: at 82 nt.
- (C) Nomination and Annotation of Domains within Predicted Polypeptide(s)
 - (D) Related Amino Acid Sequences
 - Alignment No. 13515
 - gi No. 2135765
 - % Identity 75
 - Alignment Length 12
 - Location of Alignment in SEQ ID NO 1896: from 26 to 37
 - Alignment No. 13516
 - gi No. 4505285
 - % Identity 75
 - Alignment Length 12
 - Location of Alignment in SEQ ID NO 1896: from 26 to 37

- (A) Polynucleotide Sequence
 - Pat. Appln. SEQ ID NO 1897
 - Ceres seq_id 1501632
 - (B) Polypeptide Sequence
 - Pat. Appln. SEQ ID NO 1898
 - Ceres seq_id 1501633
 - Location of start within SEQ ID NO 1897: at 2 nt.
- - (D) Related Amino Acid Sequences
 - Alignment No. 13517
 - gi No. 2204081
 - % Identity 71.4Alignment Length 14
 - Location of Alignment in SEQ ID NO 1898: from 67 to 80
 - (B) Polypeptide Sequence
 - Pat. Appln. SEQ ID NO 1899
 - Ceres seq id 1501634
 - Location of start within SEQ ID NO 1897: at 119 nt.

- (C) Nomination and Annotation of Domains within Predicted Polypeptide(s) $\label{eq:polypeptide}$
 - (D) Related Amino Acid Sequences
 - Alignment No. 13518
 - gi No. 2204081
 - % Identity 71.4
 - Alignment Length 14
 - Location of Alignment in SEQ ID NO 1899: from 28 to 41
 - (B) Polypeptide Sequence
 - Pat. Appln. SEQ ID NO 1900
 - Ceres seq id 1501635
 - Location of start within SEQ ID NO 1897: at 146 nt.
- (C) Nomination and Annotation of Domains within Predicted Polypeptide(s) $% \left(1\right) =\left(1\right) \left(1\right) +\left(1\right) \left(1\right) \left(1\right) +\left(1\right) \left(1\right)$
 - (D) Related Amino Acid Sequences
 - Alignment No. 13519
 - gi No. 2204081
 - % Identity 71.4
 - Alignment Length 14
 - Location of Alignment in SEQ ID NO 1900: from 19 to 32

- (A) Polynucleotide Sequence
 - Pat. Appln. SEQ ID NO 1901
 - Ceres seq_id 1501639
 - (B) Polypeptide Sequence
 - Pat. Appln. SEQ ID NO 1902
 - Ceres seq_id 1501640
 - Location of start within SEQ ID NO 1901: at 165 nt.
- (C) Nomination and Annotation of Domains within Predicted Polypeptide(s) $% \left(\frac{1}{2}\right) =\frac{1}{2}\left(\frac{1}{2}\right) +\frac{1}{2}\left(\frac{1}{2}\right) +\frac{$
 - (D) Related Amino Acid Sequences
 - (B) Polypeptide Sequence
 - Pat. Appln. SEQ ID NO 1903
 - Ceres seq_id 1501641
 - Location of start within SEQ ID NO 1901: at 198 nt.
- (C) Nomination and Annotation of Domains within Predicted Polypeptide(s) $% \left(\frac{1}{2}\right) =\frac{1}{2}\left(\frac{1}{2}\right) +\frac{1}{2}\left(\frac{1}{2}\right) +\frac{$
 - (D) Related Amino Acid Sequences
 - (B) Polypeptide Sequence
 - Pat. Appln. SEQ ID NO 1904
 - Ceres seq id 1501642
 - Location of start within SEQ ID NO 1901: at 362 nt.
- - (D) Related Amino Acid Sequences
 - Alignment No. 13520
 - gi No. 2894559
 - % Identity 89.1
 - Alignment Length 46
 - Location of Alignment in SEQ ID NO 1904: from 1 to 45
 - Alignment No. 13521
 - gi No. 4115936

- % Identity 87
- Alignment Length 46
- Location of Alignment in SEQ ID NO 1904: from 1 to 45

- (A) Polynucleotide Sequence
 - Pat. Appln. SEQ ID NO 1905
 - Ceres seq_id 1501643
 - (B) Polypeptide Sequence
 - Pat. Appln. SEQ ID NO 1906
 - Ceres seq_id 1501644
 - Location of start within SEQ ID NO 1905: at 2 nt.
- (C) Nomination and Annotation of Domains within Predicted Polypeptide(s)
 - Alignment No. 13522
 - Ezrin/radixin/moesin family
 - Location within SEQ ID NO 1906: from 1 to 145 aa.
 - (D) Related Amino Acid Sequences
 - (B) Polypeptide Sequence
 - Pat. Appln. SEQ ID NO 1907
 - Ceres seq_id 1501645
 - Location of start within SEQ ID NO 1905: at 167 nt.
- (C) Nomination and Annotation of Domains within Predicted Polypeptide(s) $\label{eq:continuous} % \begin{array}{c} (C) & (C)$
 - Alignment No. 13523
 - Ezrin/radixin/moesin family
 - Location within SEQ ID NO 1907: from 1 to 90 aa.
 - (D) Related Amino Acid Sequences
 - (B) Polypeptide Sequence
 - Pat. Appln. SEQ ID NO 1908
 - Ceres seq id 1501646
 - Location of start within SEQ ID NO 1905: at 399 nt.
- (C) Nomination and Annotation of Domains within Predicted Polypeptide(s) $% \left(\frac{1}{2}\right) =\frac{1}{2}\left(\frac{1}{2}\right) +\frac{1}{2}\left(\frac{1}{2}\right) +\frac{$
 - (D) Related Amino Acid Sequences

- (A) Polynucleotide Sequence
 - Pat. Appln. SEQ ID NO 1909
 - Ceres seq id 1501689
 - (B) Polypeptide Sequence
 - Pat. Appln. SEQ ID NO 1910
 - Ceres seq id 1501690
 - Location of start within SEQ ID NO 1909: at 152 nt.
- (C) Nomination and Annotation of Domains within Predicted Polypeptide(s) $% \left(\frac{1}{2}\right) =\frac{1}{2}\left(\frac{1}{2}\right) +\frac{1}{2}\left(\frac{1}{2}\right) +\frac{$
 - Alignment No. 13524
 - Ubiquitin family
 - Location within SEQ ID NO 1910: from 1 to 74 aa.
 - (D) Related Amino Acid Sequences
 - (B) Polypeptide Sequence

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- Pat. Appln. SEQ ID NO 1911
- Ceres seq id 1501691
- Location of start within SEQ ID NO 1909: at 284 nt.
- - (D) Related Amino Acid Sequences
 - (B) Polypeptide Sequence
 - Pat. Appln. SEQ ID NO 1912
 - Ceres seq id 1501692
 - Location of start within SEQ ID NO 1909: at 368 nt.
- - (D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 286738 (A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 1913
- Ceres seq_id 1501701
- (B) Polypeptide Sequence
 - Pat. Appln. SEQ ID NO 1914
 - Ceres seq_id 1501702
 - Location of start within SEQ ID NO 1913: at 3 nt.
- (C) Nomination and Annotation of Domains within Predicted Polypeptide(s) $% \left(\frac{1}{2}\right) =\frac{1}{2}\left(\frac{1}{2}\right) +\frac{1}{2}\left(\frac{1}{2}\right) +\frac{$
 - (D) Related Amino Acid Sequences
 - (B) Polypeptide Sequence
 - Pat. Appln. SEQ ID NO 1915
 - Ceres seq_id 1501703
 - Location of start within SEQ ID NO 1913: at 110 nt.
- (C) Nomination and Annotation of Domains within Predicted Polypeptide(s) $% \left(\frac{1}{2}\right) =\frac{1}{2}\left(\frac{1}{2}\right) +\frac{1}{2}\left(\frac{1}{2}\right) +\frac{$
 - (D) Related Amino Acid Sequences
 - Alignment No. 13525
 - gi No. 2244980
 - % Identity 75
 - Alignment Length 24
 - Location of Alignment in SEQ ID NO 1915: from 31 to 53
 - Alignment No. 13526
 - gi No. 4587539
 - % Identity 70
 - Alignment Length 20
 - Location of Alignment in SEQ ID NO 1915: from 31 to 50
 - Alignment No. 13527
 - gi No. 4914386
 - % Identity 70.8
 - Alignment Length 24
 - Location of Alignment in SEQ ID NO 1915: from 31 to 53

- (A) Polynucleotide Sequence
 - Pat. Appln. SEQ ID NO 1916
 - Ceres seq_id 1501710
 - (B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1917
- Ceres seq_id 1501711
- Location of start within SEQ ID NO 1916: at 2 nt.
- (C) Nomination and Annotation of Domains within Predicted Polypeptide(s)
 - Alignment No. 13528
 - Protein phosphatase 2C
 - Location within SEQ ID NO 1917: from 32 to 84 aa.
 - (D) Related Amino Acid Sequences
 - (B) Polypeptide Sequence
 - Pat. Appln. SEQ ID NO 1918
 - Ceres seq id 1501712
 - Location of start within SEQ ID NO 1916: at 295 nt.
- - Alignment No. 13529
 - Protein phosphatase 2C
 - Location within SEQ ID NO 1918: from 20 to 85 aa.
 - (D) Related Amino Acid Sequences
 - (B) Polypeptide Sequence
 - Pat. Appln. SEQ ID NO 1919
 - Ceres seq id 1501713
 - Location of start within SEQ ID NO 1916: at 346 nt.
- - Alignment No. 13530
 - Protein phosphatase 2C
 - Location within SEQ ID NO 1919: from 3 to 68 aa.
 - (D) Related Amino Acid Sequences

- (A) Polynucleotide Sequence
 - Pat. Appln. SEQ ID NO 1920
 - Ceres seq_id 1501718
 - (B) Polypeptide Sequence
 - Pat. Appln. SEQ ID NO 1921
 - Ceres seq_id 1501719
 - Location of start within SEQ ID NO 1920: at 1 nt.
- (C) Nomination and Annotation of Domains within Predicted Polypeptide(s) $\label{eq:condition} % \begin{array}{c} \text{Polyperiod} \\ \text{Poly$
 - (D) Related Amino Acid Sequences
 - Alignment No. 13531
 - gi No. 1093503
 - % Identity 81
 - Alignment Length 21
 - Location of Alignment in SEQ ID NO 1921: from 149 to 168
 - Alignment No. 13532
 - gi No. 1340178
 - % Identity 73.9
 - Alignment Length 23
 - Location of Alignment in SEQ ID NO 1921: from 147 to 168

- Alignment No. 13533 - gi No. 1498185
- % Identity 81
- Alignment Length 21
- Location of Alignment in SEQ ID NO 1921: from 149 to 168
- Alignment No. 13534
- gi No. 2146900
- % Identity 81
- Alignment Length 21
- Location of Alignment in SEQ ID NO 1921: from 149 to 168
- Alignment No. 13535
- gi No. 416764
- % Identity 76.2
- Alignment Length 21
- Location of Alignment in SEQ ID NO 1921: from 149 to 168
- Alignment No. 13536
- gi No. 416766
- % Identity 71.4
- Alignment Length 21
- Location of Alignment in SEQ ID NO 1921: from 149 to 168
- Alignment No. 13537
- gi No. 416767
- % Identity 71.4
- Alignment Length 21
- Location of Alignment in SEQ ID NO 1921: from 149 to 168
- Alignment No. 13538
- gi No. 479893
- % Identity 83.3
- Alignment Length 18
- Location of Alignment in SEQ ID NO 1921: from 149 to 166
- Alignment No. 13539
- gi No. 479895
- % Identity 77.8
- Alignment Length 18
- Location of Alignment in SEQ ID NO 1921: from 149 to 166
- (B) Polypeptide Sequence
 - Pat. Appln. SEQ ID NO 1922
 - Ceres seq_id 1501720
 - Location of start within SEQ ID NO 1920: at 49 nt.
- (C) Nomination and Annotation of Domains within Predicted Polypeptide(s) $% \left(\frac{1}{2}\right) =\frac{1}{2}\left(\frac{1}{2}\right) +\frac{1}{2}\left(\frac{1}{2}\right) +\frac{$
 - (D) Related Amino Acid Sequences
 - Alignment No. 13540
 - gi No. 1093503
 - % Identity 81
 - Alignment Length 21
 - Location of Alignment in SEQ ID NO 1922: from 133 to 152
 - Alignment No. 13541
 - gi No. 1340178
 - % Identity 73.9
 - Alignment Length 23

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- Location of Alignment in SEQ ID NO 1922: from 131 to 152
- Alignment No. 13542
- gi No. 1498185
- % Identity 81
- Alignment Length 21
- Location of Alignment in SEQ ID NO 1922: from 133 to 152
- Alignment No. 13543
- gi No. 2146900
- % Identity 81
- Alignment Length 21
- Location of Alignment in SEQ ID NO 1922: from 133 to 152
- Alignment No. 13544
- gi No. 416764
- % Identity 76.2
- Alignment Length 21
- Location of Alignment in SEQ ID NO 1922: from 133 to 152
- Alignment No. 13545
- gi No. 416766
- % Identity 71.4
- Alignment Length 21
- Location of Alignment in SEQ ID NO 1922: from 133 to 152
- Alignment No. 13546
- gi No. 416767
- % Identity 71.4
- Alignment Length 21
- Location of Alignment in SEQ ID NO 1922: from 133 to 152
- Alignment No. 13547
- gi No. 479893
- % Identity 83.3
- Alignment Length 18
- Location of Alignment in SEQ ID NO 1922: from 133 to 150
- Alignment No. 13548
- qi No. 479895
- % Identity 77.8
- Alignment Length 18
- Location of Alignment in SEQ ID NO 1922: from 133 to 150
- (B) Polypeptide Sequence
 - Pat. Appln. SEQ ID NO 1923
 - Ceres seq_id 1501721
 - Location of start within SEQ ID NO 1920: at 223 nt.
- - (D) Related Amino Acid Sequences
 - Alignment No. 13549
 - gi Ño. 1093503
 - % Identity 81
 - Alignment Length 21
 - Location of Alignment in SEQ ID NO 1923: from 75 to 94
 - Alignment No. 13550
 - gi No. 1340178
 - % Identity 73.9

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- Alignment Length 23
- Location of Alignment in SEQ ID NO 1923: from 73 to 94
- Alignment No. 13551
- gi No. 1498185
- % Identity 81
- Alignment Length 21
- Location of Alignment in SEQ ID NO 1923: from 75 to 94
- Alignment No. 13552
- gi No. 2146900
- % Identity 81
- Alignment Length 21
- Location of Alignment in SEQ ID NO 1923: from 75 to 94
- Alignment No. 13553
- gi No. 416764
- % Identity 76.2
- Alignment Length 21
- Location of Alignment in SEQ ID NO 1923: from 75 to 94
- Alignment No. 13554
- gi No. 416766
- % Identity 71.4
- Alignment Length 21
- Location of Alignment in SEQ ID NO 1923: from 75 to 94
- Alignment No. 13555
- gi No. 416767
- % Identity 71.4
- Alignment Length 21
- Location of Alignment in SEQ ID NO 1923: from 75 to 94
- Alignment No. 13556
- gi No. 479893
- % Identity 83.3
- Alignment Length 18
- Location of Alignment in SEQ ID NO 1923: from 75 to 92
- Alignment No. 13557
- gi No. 479895
- % Identity 77.8
- Alignment Length 18
- Location of Alignment in SEQ ID NO 1923: from 75 to 92

- (A) Polynucleotide Sequence
 - Pat. Appln. SEQ ID NO 1924
 - Ceres seq_id 1501722
 - (B) Polypeptide Sequence
 - Pat. Appln. SEQ ID NO 1925
 - Ceres seq id 1501723
 - Location of start within SEQ ID NO 1924: at 2 nt.
- - (D) Related Amino Acid Sequences
 - (B) Polypeptide Sequence
 - Pat. Appln. SEQ ID NO 1926
 - Ceres seq_id 1501724

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- Location of start within SEQ ID NO 1924: at 41 nt.
- - (D) Related Amino Acid Sequences
 - (B) Polypeptide Sequence
 - Pat. Appln. SEQ ID NO 1927
 - Ceres seg id 1501725
 - Location of start within SEQ ID NO 1924: at 312 nt.
- - Alignment No. 13558
 - RNA recognition motif. (a.k.a. RRM, RBD, or RNP domain)
 - Location within SEQ ID NO 1927: from 1 to 55 aa.
 - (D) Related Amino Acid Sequences

- (A) Polynucleotide Sequence
 - Pat. Appln. SEQ ID NO 1928
 - Ceres seq id 1501730
 - (B) Polypeptide Sequence
 - Pat. Appln. SEQ ID NO 1929
 - Ceres seq_id 1501731
 - Location of start within SEQ ID NO 1928: at 137 nt.
- - Alignment No. 13559
 - Collagen triple helix repeat (20 copies)
 - Location within SEQ ID NO 1929: from 33 to 96 aa.
 - Alignment No. 13560
 - Collagen triple helix repeat (20 copies)
 - Location within SEQ ID NO 1929: from 45 to 102 aa.
 - Alignment No. 13561
 - Collagen triple helix repeat (20 copies)
 - Location within SEQ ID NO 1929: from 45 to 106 aa.
 - Alignment No. 13562
 - Collagen triple helix repeat (20 copies)
 - Location within SEQ ID NO 1929: from 62 to 108 aa.
 - Alignment No. 13563
 - 7 transmembrane receptor (rhodopsin family)
 - Location within SEQ ID NO 1929: from 32 to 100 aa.
 - Alignment No. 13564
 - 7 transmembrane receptor (rhodopsin family)
 - Location within SEQ ID NO 1929: from 32 to 106 aa.
 - Alignment No. 13565
 - 7 transmembrane receptor (rhodopsin family)
 - Location within SEQ ID NO 1929: from 32 to 108 aa.
 - Alignment No. 13566
 - 7 transmembrane receptor (rhodopsin family)
 - Location within SEQ ID NO 1929: from 33 to 94 aa.

- Alignment No. 13567
- 7 transmembrane receptor (rhodopsin family)
- Location within SEQ ID NO 1929: from 33 to 106 aa.
- Alignment No. 13568
- 7 transmembrane receptor (rhodopsin family)
- Location within SEQ ID NO 1929: from 33 to 108 aa.
- (D) Related Amino Acid Sequences
- (B) Polypeptide Sequence
 - Pat. Appln. SEQ ID NO 1930
 - Ceres seq_id 1501732
 - Location of start within SEQ ID NO 1928: at 347 nt.
- - (D) Related Amino Acid Sequences
 - (B) Polypeptide Sequence
 - Pat. Appln. SEQ ID NO 1931
 - Ceres seg id 1501733
 - Location of start within SEQ ID NO 1928: at 389 nt.
- (C) Nomination and Annotation of Domains within Predicted Polypeptide(s)
 - (D) Related Amino Acid Sequences

- (A) Polynucleotide Sequence
 - Pat. Appln. SEQ ID NO 1932
 - Ceres seq_id 1501737
 - (B) Polypeptide Sequence
 - Pat. Appln. SEQ ID NO 1933
 - Ceres seq_id 1501738
 - Location of start within SEQ ID NO 1932: at 1 nt.
- - (D) Related Amino Acid Sequences
 - (B) Polypeptide Sequence
 - Pat. Appln. SEQ ID NO 1934
 - Ceres seq_id 1501739
 - Location of start within SEQ ID NO 1932: at 2 nt.
- (C) Nomination and Annotation of Domains within Predicted Polypeptide(s) $% \left(\frac{1}{2}\right) =\frac{1}{2}\left(\frac{1}{2}\right) +\frac{1}{2}\left(\frac{1}{2}\right) +\frac{$
 - Alignment No. 13569
 - Collagen triple helix repeat (20 copies)
 - Location within SEQ ID NO 1934: from 34 to 83 aa.
 - Alignment No. 13570
 - 7 transmembrane receptor (rhodopsin family)
 - Location within SEQ ID NO 1934: from 5 to 83 aa.
 - Alignment No. 13571
 - 7 transmembrane receptor (rhodopsin family)
 - Location within SEQ ID NO 1934: from 21 to 83 aa.

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- (D) Related Amino Acid Sequences
 - Alignment No. 13572
 - gi No. 3327046
 - % Identity 70.6
 - Alignment Length 17
 - Location of Alignment in SEQ ID NO 1934: from 67 to 83
 - Alignment No. 13573
 - gi No. 3745837
 - % Identity 75
 - Alignment Length 20
 - Location of Alignment in SEQ ID NO 1934: from 65 to 83
 - Alignment No. 13574
 - gi No. 4028930
 - % Identity 70.6
 - Alignment Length 17
 - Location of Alignment in SEQ ID NO 1934: from 67 to 83
 - Alignment No. 13575
 - gi No. 4775349
 - % Identity 81.8
 - Alignment Length 11
 - Location of Alignment in SEQ ID NO 1934: from 72 to 82
 - Alignment No. 13576
 - gi No. 4775349
 - % Identity 83.3
 - Alignment Length 12
 - Location of Alignment in SEQ ID NO 1934: from 72 to 82
 - Alignment No. 13577
 - gi No. 4996894
 - % Identity 81.8
 - Alignment Length 11
 - Location of Alignment in SEQ ID NO 1934: from 72 to 82
 - Alignment No. 13578
 - gi No. 4996894
 - % Identity 83.3
 - Alignment Length 12
 - Location of Alignment in SEQ ID NO 1934: from 72 to 82
 - Alignment No. 13579
 - gi No. 688080
 - % Identity 80
 - Alignment Length 15
 - Location of Alignment in SEQ ID NO 1934: from 65 to 78
- (B) Polypeptide Sequence
 - Pat. Appln. SEQ ID NO 1935
 - Ceres seq id 1501740
 - Location of start within SEQ ID NO 1932: at 64 nt.
- (C) Nomination and Annotation of Domains within Predicted Polypeptide(s)
 - (D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 287760 (A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 1936

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- Ceres seq id 1501741
- (B) Polypeptide Sequence
 - Pat. Appln. SEQ ID NO 1937
 - Ceres seq_id 1501742
 - Location of start within SEQ ID NO 1936: at 1 nt.
- - Alignment No. 13580
 - DnaJ domain
 - Location within SEQ ID NO 1937: from 36 to 81 aa.
 - (D) Related Amino Acid Sequences
 - Alignment No. 13581
 - gi No. 1125691
 - % Identity 84.5
 - Alignment Length 58
 - Location of Alignment in SEQ ID NO 1937: from 24 to 81
 - Alignment No. 13582
 - qi No. 1169382
 - % Identity 82.8
 - Alignment Length 58
 - Location of Alignment in SEQ ID NO 1937: from 24 to 81
 - Alignment No. 13583
 - gi No. 1169383
 - % Identity 76.3
 - Alignment Length 59
 - Location of Alignment in SEQ ID NO 1937: from 24 to 81
 - Alignment No. 13584
 - gi No. 1169384
 - % Identity 86.2
 - Alignment Length 58
 - Location of Alignment in SEQ ID NO 1937: from 24 to 81
 - Alignment No. 13585
 - gi No. 2129577
 - % Identity 79.7
 - Alignment Length 59
 - Location of Alignment in SEQ ID NO 1937: from 24 to 81
 - Alignment No. 13586
 - gi No. 2370312
 - % Identity 78
 - Alignment Length 59
 - Location of Alignment in SEQ ID NO 1937: from 24 to 81
 - Alignment No. 13587
 - gi No. 2641638
 - % Identity 79.7
 - Alignment Length 59
 - Location of Alignment in SEQ ID NO 1937: from 24 to 81
 - Alignment No. 13588
 - gi No. 2984709
 - % Identity 89.7
 - Alignment Length 58
 - Location of Alignment in SEQ ID NO 1937: from 24 to 81

- Alignment No. 13589 - gi No. 39890 - % Identity 73.7 - Alignment Length 19 - Location of Alignment in SEQ ID NO 1937: from 37 to 55 - Alignment No. 13590 - gi No. 4008159 - % Identity 89.7 - Alignment Length 58 - Location of Alignment in SEQ ID NO 1937: from 24 to 81 - Alignment No. 13591 - gi No. 4097575 - % Identity 86.2 - Alignment Length 58 - Location of Alignment in SEQ ID NO 1937: from 24 to 81 - Alignment No. 13592 - gi No. 4097577 - % Identity 82.8 - Alignment Length 58 - Location of Alignment in SEQ ID NO 1937: from 24 to 81 - Alignment No. 13593 - gi No. 4210948 - % Identity 91.4 - Alignment Length 58 - Location of Alignment in SEQ ID NO 1937: from 24 to 81 - Alignment No. 13594 - gi No. 421809 - % Identity 89.7 - Alignment Length 58 - Location of Alignment in SEQ ID NO 1937: from 24 to 81 - Alignment No. 13595 - gi No. 4589726 - % Identity 81 - Alignment Length 58 - Location of Alignment in SEQ ID NO 1937: from 24 to 81 - Alignment No. 13596 - qi No. 461942 - % Identity 86.5 - Alignment Length 37 - Location of Alignment in SEQ ID NO 1937: from 45 to 81 - Alignment No. 13597 - gi No. 461944 - % Identity 89.7 - Alignment Length 58 - Location of Alignment in SEQ ID NO 1937: from 24 to 81
- (C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Location of start within SEQ ID NO 1936: at 2 nt.

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1938

- Ceres seq_id 1501743

(D) Related Amino Acid Sequences

- (B) Polypeptide Sequence
 - Pat. Appln. SEQ ID NO 1939
 - Ceres seq_id 1501744
 - Location of start within SEQ ID NO 1936: at 70 nt.
- (C) Nomination and Annotation of Domains within Predicted Polypeptide(s)
 - Alignment No. 13598
 - DnaJ domain
 - Location within SEQ ID NO 1939: from 13 to 58 aa.
 - (D) Related Amino Acid Sequences
 - Alignment No. 13599
 - gi No. 1125691
 - % Identity 84.5
 - Alignment Length 58
 - Location of Alignment in SEQ ID NO 1939: from 1 to 58
 - Alignment No. 13600
 - gi No. 1169382
 - % Identity 82.8
 - Alignment Length 58
 - Location of Alignment in SEQ ID NO 1939: from 1 to 58
 - Alignment No. 13601
 - gi No. 1169383
 - % Identity 76.3
 - Alignment Length 59
 - Location of Alignment in SEQ ID NO 1939: from 1 to 58
 - Alignment No. 13602
 - gi No. 1169384
 - % Identity 86.2
 - Alignment Length 58
 - Location of Alignment in SEQ ID NO 1939: from 1 to 58
 - Alignment No. 13603
 - gi No. 2129577
 - % Identity 79.7
 - Alignment Length 59
 - Location of Alignment in SEQ ID NO 1939: from 1 to 58
 - Alignment No. 13604
 - gi No. 2370312
 - % Identity 78
 - Alignment Length 59
 - Location of Alignment in SEQ ID NO 1939: from 1 to 58
 - Alignment No. 13605
 - gi No. 2641638
 - % Identity 79.7
 - Alignment Length 59
 - Location of Alignment in SEQ ID NO 1939: from 1 to 58
 - Alignment No. 13606
 - gi No. 2984709
 - % Identity 89.7
 - Alignment Length 58
 - Location of Alignment in SEQ ID NO 1939: from 1 to 58

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- Alignment No. 13607
- gi No. 39890
- % Identity 73.7
- Alignment Length 19
- Location of Alignment in SEQ ID NO 1939: from 14 to 32
- Alignment No. 13608
- gi No. 4008159
- % Identity 89.7
- Alignment Length 58
- Location of Alignment in SEQ ID NO 1939: from 1 to 58
- Alignment No. 13609
- gi No. 4097575
- % Identity 86.2
- Alignment Length 58
- Location of Alignment in SEQ ID NO 1939: from 1 to 58
- Alignment No. 13610
- gi No. 4097577
- % Identity 82.8
- Alignment Length 58
- Location of Alignment in SEQ ID NO 1939: from 1 to 58
- Alignment No. 13611
- gi No. 4210948
- % Identity 91.4
- Alignment Length 58
- Location of Alignment in SEQ ID NO 1939: from 1 to 58
- Alignment No. 13612
- qi No. 421809
- % Identity 89.7
- Alignment Length 58
- Location of Alignment in SEQ ID NO 1939: from 1 to 58
- Alignment No. 13613
- gi No. 4589726
- % Identity 81
- Alignment Length 58
- Location of Alignment in SEQ ID NO 1939: from 1 to 58
- Alignment No. 13614
- gi No. 461942
- % Identity 86.5
- Alignment Length 37
- Location of Alignment in SEQ ID NO 1939: from 22 to 58
- Alignment No. 13615
- gi No. 461944
- % Identity 89.7
- Alignment Length 58
- Location of Alignment in SEQ ID NO 1939: from 1 to 58
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- (A) Polynucleotide Sequence
 - Pat. Appln. SEQ ID NO 1940
 - Ceres seq_id 1501755
 - (B) Polypeptide Sequence
 - Pat. Appln. SEQ ID NO 1941

- Ceres seq id 1501756
- Location of start within SEQ ID NO 1940: at 3 nt.
- (C) Nomination and Annotation of Domains within Predicted Polypeptide(s)
 - (D) Related Amino Acid Sequences
 - (B) Polypeptide Sequence
 - Pat. Appln. SEQ ID NO 1942
 - Ceres seq_id 1501757
 - Location of start within SEQ ID NO 1940: at 155 nt.
- - (D) Related Amino Acid Sequences
 - (B) Polypeptide Sequence
 - Pat. Appln. SEQ ID NO 1943
 - Ceres seq id 1501758
 - Location of start within SEQ ID NO 1940: at 207 nt.
- - (D) Related Amino Acid Sequences
 - Alignment No. 13616
 - gi No. 2342735
 - % Identity 81.8
 - Alignment Length 55
 - Location of Alignment in SEQ ID NO 1943: from 37 to 91

- (A) Polynucleotide Sequence
 - Pat. Appln. SEQ ID NO 1944
 - Ceres seq_id 1501763
 - (B) Polypeptide Sequence
 - Pat. Appln. SEQ ID NO 1945
 - Ceres seg id 1501764
 - Location of start within SEQ ID NO 1944: at 2 nt.
- (C) Nomination and Annotation of Domains within Predicted Polypeptide(s) $% \left(1\right) =\left(1\right) \left(1\right) +\left(1\right) \left(1\right) \left(1\right) +\left(1\right) \left(1\right)$
 - Alignment No. 13617
 - Ribosomal protein L14
 - Location within SEQ ID NO 1945: from 28 to 149 aa.
 - (D) Related Amino Acid Sequences
 - Alignment No. 13618
 - gi No. 103355
 - % Identity 79.9
 - Alignment Length 139
 - Location of Alignment in SEQ ID NO 1945: from 10 to 148
 - Alignment No. 13619
 - gi No. 132744
 - % Identity 75.9
 - Alignment Length 133
 - Location of Alignment in SEQ ID NO 1945: from 17 to 149
 - Alignment No. 13620
 - gi No. 1350671
 - % Identity 74.8

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- Alignment Length 139
- Location of Alignment in SEQ ID NO 1945: from 10 to 148
- Alignment No. 13621
- gi No. 1350673
- % Identity 77
- Alignment Length 139
- Location of Alignment in SEQ ID NO 1945: from 10 to 148
- Alignment No. 13622
- gi No. 1710495
- % Identity 95.4
- Alignment Length 87
- Location of Alignment in SEQ ID NO 1945: from 10 to 96
- Alignment No. 13623
- gi No. 1710496
- % Identity 75
- Alignment Length 48
- Location of Alignment in SEQ ID NO 1945: from 10 to 57
- Alignment No. 13624
- gi No. 2341028
- % Identity 96.3
- Alignment Length 136
- Location of Alignment in SEQ ID NO 1945: from 14 to 149
- Alignment No. 13625
- gi No. 2459420
- % Identity 96.4
- Alignment Length 140
- Location of Alignment in SEQ ID NO 1945: from 10 to 149
- Alignment No. 13626
- gi No. 2500265
- % Identity 77
- Alignment Length 139
- Location of Alignment in SEQ ID NO 1945: from 10 to 148
- Alignment No. 13627
- gi No. 2706454
- % Identity 77.4
- Alignment Length 137
- Location of Alignment in SEQ ID NO 1945: from 13 to 149
- Alignment No. 13628
- gi No. 279650
- % Identity 82.7
- Alignment Length 139
- Location of Alignment in SEQ ID NO 1945: from 10 to 148
- Alignment No. 13629
- gi No. 2982289
- % Identity 99.2
- Alignment Length 133
- Location of Alignment in SEQ ID NO 1945: from 17 to 149
- Alignment No. 13630
- gi No. 3851618
- % Identity 74.6
- Alignment Length 130

- Location of Alignment in SEQ ID NO 1945: from 20 to 149
- Alignment No. 13631
- gi No. 4028025
- % Identity 83.2
- Alignment Length 125
- Location of Alignment in SEQ ID NO 1945: from 14 to 138
- Alignment No. 13632
- gi No. 4506605
- % Identity 83.5
- Alignment Length 139
- Location of Alignment in SEQ ID NO 1945: from 10 to 148
- Alignment No. 13633
- gi No. 4574244
- % Identity 90
- Alignment Length 140
- Location of Alignment in SEQ ID NO 1945: from 10 to 149
- Alignment No. 13634
- gi No. 4583511
- % Identity 82.7
- Alignment Length 139
- Location of Alignment in SEQ ID NO 1945: from 10 to 148
- Alignment No. 13635
- gi No. 5441537
- % Identity 82.7
- Alignment Length 139
- Location of Alignment in SEQ ID NO 1945: from 10 to 148
- Alignment No. 13636
- gi No. 546005
- % Identity 75.5
- Alignment Length 49
- Location of Alignment in SEQ ID NO 1945: from 10 to 58
- Alignment No. 13637
- gi No. 730536
- % Identity 96.4
- Alignment Length 140
- Location of Alignment in SEQ ID NO 1945: from 10 to 149
- (B) Polypeptide Sequence
 - Pat. Appln. SEQ ID NO 1946
 - Ceres seq_id 1501765
 - Location of start within SEQ ID NO 1944: at 29 nt.
- (C) Nomination and Annotation of Domains within Predicted Polypeptide(s) $\label{eq:polypeptide} % \begin{array}{c} (C) & (C$
 - Alignment No. 13638
 - Ribosomal protein L14
 - Location within SEQ ID NO 1946: from 19 to 140 aa.
 - (D) Related Amino Acid Sequences
 - Alignment No. 13639
 - gi No. 103355
 - % Identity 79.9
 - Alignment Length 139
 - Location of Alignment in SEQ ID NO 1946: from 1 to 139

- Alignment No. 13640
- gi No. 132744
- % Identity 75.9
- Alignment Length 133
- Location of Alignment in SEQ ID NO 1946: from 8 to 140
- Alignment No. 13641
- gi No. 1350671
- % Identity 74.8
- Alignment Length 139
- Location of Alignment in SEQ ID NO 1946: from 1 to 139
- Alignment No. 13642
- gi No. 1350673
- % Identity 77
- Alignment Length 139
- Location of Alignment in SEQ ID NO 1946: from 1 to 139
- Alignment No. 13643
- gi No. 1710495
- % Identity 95.4
- Alignment Length 87
- Location of Alignment in SEQ ID NO 1946: from 1 to 87
- Alignment No. 13644
- gi No. 1710496
- % Identity 75
- Alignment Length 48
- Location of Alignment in SEQ ID NO 1946: from 1 to 48
- Alignment No. 13645
- gi No. 2341028
- % Identity 96.3
- Alignment Length 136
- Location of Alignment in SEQ ID NO 1946: from 5 to 140 $\,$
- Alignment No. 13646
- gi No. 2459420
- % Identity 96.4
- Alignment Length 140
- Location of Alignment in SEQ ID NO 1946: from 1 to 140
- Alignment No. 13647
- gi No. 2500265
- % Identity 77
- Alignment Length 139
- Location of Alignment in SEQ ID NO 1946: from 1 to 139
- Alignment No. 13648
- gi No. 2706454
- % Identity 77.4
- Alignment Length 137
- Location of Alignment in SEQ ID NO 1946: from 4 to 140
- Alignment No. 13649
- gi No. 279650
- % Identity 82.7
- Alignment Length 139
- Location of Alignment in SEQ ID NO 1946: from 1 to 139

- Alignment No. 13650 - gi No. 2982289 - % Identity 99.2 - Alignment Length 133 - Location of Alignment in SEQ ID NO 1946: from 8 to 140 - Alignment No. 13651 - gi No. 3851618 - % Identity 74.6 - Alignment Length 130 - Location of Alignment in SEQ ID NO 1946: from 11 to 140 - Alignment No. 13652 - gi No. 4028025 - % Identity 83.2 - Alignment Length 125 - Location of Alignment in SEQ ID NO 1946: from 5 to 129 - Alignment No. 13653 - gi No. 4506605 - % Identity 83.5 - Alignment Length 139 - Location of Alignment in SEQ ID NO 1946: from 1 to 139 - Alignment No. 13654 - gi No. 4574244 - % Identity 90 - Alignment Length 140 - Location of Alignment in SEQ ID NO 1946: from 1 to 140 $\,$ - Alignment No. 13655 - gi No. 4583511 - % Identity 82.7 - Alignment Length 139 - Location of Alignment in SEQ ID NO 1946: from 1 to 139 - Alignment No. 13656 - gi No. 5441537 - % Identity 82.7 - Alignment Length 139 - Location of Alignment in SEQ ID NO 1946: from 1 to 139 - Alignment No. 13657 - gi No. 546005 - % Identity 75.5 - Alignment Length 49 - Location of Alignment in SEQ ID NO 1946: from 1 to 49 - Alignment No. 13658 - gi No. 730536 - % Identity 96.4 - Alignment Length 140 - Location of Alignment in SEQ ID NO 1946: from 1 to 140
- (B) Polypeptide Sequence
 - Pat. Appln. SEQ ID NO 1947
 - Ceres seq_id 1501766
 - Location of start within SEQ ID NO 1944: at 74 nt.
- (C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 13659
- Ribosomal protein L14
- Location within SEQ ID NO 1947: from 4 to 125 aa.
- (D) Related Amino Acid Sequences
 - Alignment No. 13660
 - gi No. 103355
 - % Identity 79.9
 - Alignment Length 139
 - Location of Alignment in SEQ ID NO 1947: from 1 to 124
 - Alignment No. 13661
 - gi No. 132744
 - % Identity 75.9
 - Alignment Length 133
 - Location of Alignment in SEQ ID NO 1947: from 1 to 125
 - Alignment No. 13662
 - gi No. 1350671
 - % Identity 74.8
 - Alignment Length 139
 - Location of Alignment in SEQ ID NO 1947: from 1 to 124
 - Alignment No. 13663
 - gi No. 1350673
 - % Identity 77
 - Alignment Length 139
 - Location of Alignment in SEQ ID NO 1947: from 1 to 124
 - Alignment No. 13664
 - gi No. 1710495
 - % Identity 95.4
 - Alignment Length 87
 - Location of Alignment in SEQ ID NO 1947: from 1 to 72
 - Alignment No. 13665
 - gi No. 1710496
 - % Identity 75
 - Alignment Length 48
 - Location of Alignment in SEQ ID NO 1947: from 1 to 33
 - Alignment No. 13666
 - gi No. 2341028
 - % Identity 96.3
 - Alignment Length 136
 - Location of Alignment in SEQ ID NO 1947: from 1 to 125
 - Alignment No. 13667
 - gi No. 2459420
 - % Identity 96.4
 - Alignment Length 140
 - Location of Alignment in SEQ ID NO 1947: from 1 to 125
 - Alignment No. 13668
 - gi No. 2500265
 - % Identity 77
 - Alignment Length 139
 - Location of Alignment in SEQ ID NO 1947: from 1 to 124
 - Alignment No. 13669
 - gi No. 2706454

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- % Identity 77.4 - Alignment Length 137 - Location of Alignment in SEQ ID NO 1947: from 1 to 125 - Alignment No. 13670 - qi No. 279650 - % Identity 82.7 - Alignment Length 139 - Location of Alignment in SEQ ID NO 1947: from 1 to 124 - Alignment No. 13671 - gi No. 2982289 - % Identity 99.2 - Alignment Length 133 - Location of Alignment in SEQ ID NO 1947: from 1 to 125 - Alignment No. 13672 - gi No. 3851618 - % Identity 74.6 - Alignment Length 130 - Location of Alignment in SEQ ID NO 1947: from 1 to 125 - Alignment No. 13673 - gi No. 4028025 - % Identity 83.2 - Alignment Length 125 - Location of Alignment in SEQ ID NO 1947: from 1 to 114
- Alignment No. 13674 - gi No. 4506605
- % Identity 83.5 - Alignment Length 139
- Location of Alignment in SEQ ID NO 1947: from 1 to 124
- Alignment No. 13675
- gi No. 4574244
- % Identity 90
- Alignment Length 140
- Location of Alignment in SEQ ID NO 1947: from 1 to 125
- Alignment No. 13676
- qi No. 4583511
- % Identity 82.7
- Alignment Length 139
- Location of Alignment in SEQ ID NO 1947: from 1 to 124
- Alignment No. 13677
- gi No. 5441537
- % Identity 82.7
- Alignment Length 139
- Location of Alignment in SEQ ID NO 1947: from 1 to 124
- Alignment No. 13678
- gi No. 546005
- % Identity 75.5
- Alignment Length 49
- Location of Alignment in SEQ ID NO 1947: from 1 to 34
- Alignment No. 13679
- gi No. 730536
- % Identity 96.4

Alignment Length 140
 Location of Alignment in SEQ ID NO 1947: from 1 to 125

Maximum Length Sequence corresponding to clone ID 288149

- (A) Polynucleotide Sequence
 - Pat. Appln. SEQ ID NO 1948
 - Ceres seq id 1501771
 - (B) Polypeptide Sequence
 - Pat. Appln. SEQ ID NO 1949
 - Ceres seq_id 1501772
 - Location of start within SEQ ID NO 1948: at 1 nt.
- (C) Nomination and Annotation of Domains within Predicted Polypeptide(s) $\label{eq:condition}$
 - Alignment No. 13680
 - Eukaryotic protein kinase domain
 - Location within SEQ ID NO 1949: from 88 to 176 aa.
 - (D) Related Amino Acid Sequences
 - (B) Polypeptide Sequence
 - Pat. Appln. SEQ ID NO 1950
 - Ceres seq_id 1501773
 - Location of start within SEQ ID NO 1948: at 136 nt.
- - Alignment No. 13681
 - Eukaryotic protein kinase domain
 - Location within SEQ ID NO 1950: from 43 to 131 aa.
 - (D) Related Amino Acid Sequences
 - (B) Polypeptide Sequence
 - Pat. Appln. SEQ ID NO 1951
 - Ceres seq_id 1501774
 - Location of start within SEQ ID NO 1948: at 241 nt.
- (C) Nomination and Annotation of Domains within Predicted Polypeptide(s)
 - Alignment No. 13682
 - Eukaryotic protein kinase domain
 - Location within SEQ ID NO 1951: from 8 to 96 aa.
 - (D) Related Amino Acid Sequences

- (A) Polynucleotide Sequence
 - Pat. Appln. SEQ ID NO 1952
 - Ceres seq_id 1501786
 - (B) Polypeptide Sequence
 - Pat. Appln. SEQ ID NO 1953
 - Ceres seq_id 1501787
 - Location of start within SEQ ID NO 1952: at 1 nt.
- - (D) Related Amino Acid Sequences
 - Alignment No. 13683
 - gi No. 1184100
 - % Identity 90.9

- Alignment Length 11
- Location of Alignment in SEQ ID NO 1953: from 40 to 50
- Alignment No. 13684
- qi No. 1914851
- % Identity 72.7
- Alignment Length 11
- Location of Alignment in SEQ ID NO 1953: from 41 to 51
- Alignment No. 13685
- gi No. 688080
- % Identity 72.7
- Alignment Length 11
- Location of Alignment in SEQ ID NO 1953: from 40 to 50
- (B) Polypeptide Sequence
 - Pat. Appln. SEQ ID NO 1954
 - Ceres seq_id 1501788
 - Location of start within SEQ ID NO 1952: at 2 nt.
- (C) Nomination and Annotation of Domains within Predicted Polypeptide(s)
 - (D) Related Amino Acid Sequences
 - Alignment No. 13686
 - gi No. 19917
 - % Identity 75
 - Alignment Length 12
 - Location of Alignment in SEQ ID NO 1954: from 30 to 40
 - Alignment No. 13687
 - gi No. 322760
 - % Identity 72.7
 - Alignment Length 11
 - Location of Alignment in SEQ ID NO 1954: from 30 to 40
 - (B) Polypeptide Sequence
 - Pat. Appln. SEQ ID NO 1955
 - Ceres seq_id 1501789
 - Location of start within SEQ ID NO 1952: at 26 nt.
- - (D) Related Amino Acid Sequences
 - Alignment No. 13688
 - gi No. 19917
 - % Identity 75
 - Alignment Length 12
 - Location of Alignment in SEQ ID NO 1955: from 22 to 32
 - Alignment No. 13689
 - gi No. 322760
 - % Identity 72.7
 - Alignment Length 11
 - Location of Alignment in SEQ ID NO 1955: from 22 to 32

- (A) Polynucleotide Sequence
 - Pat. Appln. SEQ ID NO 1956
 - Ceres seq id 1501794
 - (B) Polypeptide Sequence
 - Pat. Appln. SEQ ID NO 1957

- Ceres seq_id 1501795
- Location of start within SEQ ID NO 1956: at 3 nt.
- (C) Nomination and Annotation of Domains within Predicted Polypeptide(s)
 - (D) Related Amino Acid Sequences
 - (B) Polypeptide Sequence
 - Pat. Appln. SEQ ID NO 1958
 - Ceres seq id 1501796
 - Location of start within SEQ ID NO 1956: at 182 nt.
- - (D) Related Amino Acid Sequences
 - Alignment No. 13690
 - gi No. 4521249
 - % Identity 71
 - Alignment Length 107
 - Location of Alignment in SEQ ID NO 1958: from 1 to 92
 - Alignment No. 13691
 - gi No. 4587311
 - % Identity 71
 - Alignment Length 107
 - Location of Alignment in SEQ ID NO 1958: from 1 to 92
 - Alignment No. 13692
 - gi No. 4929561
 - % Identity 71
 - Alignment Length 107
 - Location of Alignment in SEQ ID NO 1958: from 1 to 92
 - (B) Polypeptide Sequence
 - Pat. Appln. SEQ ID NO 1959
 - Ceres seq_id 1501797
 - Location of start within SEQ ID NO 1956: at 209 nt.
- (C) Nomination and Annotation of Domains within Predicted Polypeptide(s) $\label{eq:continuous}$
 - (D) Related Amino Acid Sequences
 - Alignment No. 13693
 - gi No. 4521249
 - % Identity 71
 - Alignment Length 107
 - Location of Alignment in SEQ ID NO 1959: from 1 to 83
 - Alignment No. 13694
 - gi No. 4587311
 - % Identity 71
 - Alignment Length 107
 - Location of Alignment in SEQ ID NO 1959: from 1 to 83
 - Alignment No. 13695
 - qi No. 4929561
 - % Identity 71
 - Alignment Length 107
 - Location of Alignment in SEQ ID NO 1959: from 1 to 83

Maximum Length Sequence corresponding to clone ID 288752 (A) Polynucleotide Sequence

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- Pat. Appln. SEQ ID NO 1960
- Ceres seq_id 1501804
- (B) Polypeptide Sequence
 - Pat. Appln. SEQ ID NO 1961
 - Ceres seq_id 1501805
 - Location of start within SEQ ID NO 1960: at 1 nt.
- (C) Nomination and Annotation of Domains within Predicted Polypeptide(s)
 - (D) Related Amino Acid Sequences
 - Alignment No. 13696
 - gi No. 1076501
 - % Identity 75
 - Alignment Length 12
 - Location of Alignment in SEQ ID NO 1961: from 62 to 73
 - Alignment No. 13697
 - gi No. 1076501
 - % Identity 76.9
 - Alignment Length 13
 - Location of Alignment in SEQ ID NO 1961: from 62 to 73
 - Alignment No. 13698
 - gi No. 1155068
 - % Identity 71.4
 - Alignment Length 14
 - Location of Alignment in SEQ ID NO 1961: from 62 to 73
 - Alignment No. 13699
 - gi No. 1155068
 - % Identity 71.4
 - Alignment Length 14
 - Location of Alignment in SEQ ID NO 1961: from 62 to 73
 - Alignment No. 13700
 - gi No. 1155068
 - % Identity 70.6
 - Alignment Length 17
 - Location of Alignment in SEQ ID NO 1961: from 62 to 74
 - Alignment No. 13701
 - gi No. 1155068
 - % Identity 70.6
 - Alignment Length 17
 - Location of Alignment in SEQ ID NO 1961: from 62 to 74
 - Alignment No. 13702
 - gi No. 2226329
 - % Identity 84.7
 - Alignment Length 59
 - Location of Alignment in SEQ ID NO 1961: from 34 to 91
 - Alignment No. 13703
 - gi No. 399204
 - % Identity 86.4
 - Alignment Length 59
 - Location of Alignment in SEQ ID NO 1961: from 34 to 91
 - Alignment No. 13704
 - gi No. 688422
 - % Identity 71.4

- Alignment Length 14
- Location of Alignment in SEQ ID NO 1961: from 79 to 91
- (B) Polypeptide Sequence
 - Pat. Appln. SEQ ID NO 1962
 - Ceres seq id 1501806
 - Location of start within SEQ ID NO 1960: at 3 nt.
- - Alignment No. 13705
 - Plant lipid transfer protein family
 - Location within SEQ ID NO 1962: from 81 to 137 aa.
 - (D) Related Amino Acid Sequences
 - Alignment No. 13706
 - gi No. 1092083
 - % Identity 76.5
 - Alignment Length 17
 - Location of Alignment in SEQ ID NO 1962: from 112 to 128
 - Alignment No. 13707
 - gi No. 2226329
 - % Identity 82
 - Alignment Length 50
 - Location of Alignment in SEQ ID NO 1962: from 89 to 136
 - Alignment No. 13708
 - gi No. 399204
 - % Identity 81.6
 - Alignment Length 49
 - Location of Alignment in SEQ ID NO 1962: from 89 to 137
 - (B) Polypeptide Sequence
 - Pat. Appln. SEQ ID NO 1963
 - Ceres seq_id 1501807
 - Location of start within SEQ ID NO 1960: at 158 nt.
- - (D) Related Amino Acid Sequences

- (A) Polynucleotide Sequence
 - Pat. Appln. SEQ ID NO 1964
 - Ceres seq_id 1501810
 - (B) Polypeptide Sequence
 - Pat. Appln. SEQ ID NO 1965
 - Ceres seq_id 1501811
 - Location of start within SEQ ID NO 1964: at 115 nt.
- (C) Nomination and Annotation of Domains within Predicted Polypeptide(s) $% \left(\frac{1}{2}\right) =\frac{1}{2}\left(\frac{1}{2}\right) +\frac{1}{2}\left(\frac{1}{2}\right) +\frac{$
 - (D) Related Amino Acid Sequences
 - Alignment No. 13709
 - gi No. 1076418
 - % Identity 77
 - Alignment Length 100
 - Location of Alignment in SEQ ID NO 1965: from 11 to 109
 - Alignment No. 13710

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- qi No. 1717779
- % Identity 70.3
- Alignment Length 101
- Location of Alignment in SEQ ID NO 1965: from 9 to 109
- Alignment No. 13711
- gi No. 1942055
- % Identity 77
- Alignment Length 100
- Location of Alignment in SEQ ID NO 1965: from 11 to 109
- Alignment No. 13712
- gi No. 2262173
- % Identity 72.3
- Alignment Length 101
- Location of Alignment in SEQ ID NO 1965: from 10 to 109
- Alignment No. 13713
- gi No. 2500128
- % Identity 70.2
- Alignment Length 94
- Location of Alignment in SEQ ID NO 1965: from 12 to 105
- Alignment No. 13714
- gi No. 2500129
- % Identity 71
- Alignment Length 100
- Location of Alignment in SEQ ID NO 1965: from 11 to 109
- Alignment No. 13715
- gi No. 2500130
- % Identity 70.1
- Alignment Length 77
- Location of Alignment in SEQ ID NO 1965: from 34 to 109
- (B) Polypeptide Sequence
 - Pat. Appln. SEQ ID NO 1966
 - Ceres seq_id 1501812
 - Location of start within SEQ ID NO 1964: at 241 nt.
- (C) Nomination and Annotation of Domains within Predicted Polypeptide(s)
 - (D) Related Amino Acid Sequences
 - Alignment No. 13716
 - gi No. 1076418
 - % Identity 77
 - Alignment Length 100
 - Location of Alignment in SEQ ID NO 1966: from 1 to 67
 - Alignment No. 13717
 - gi No. 1717779
 - % Identity 70.3
 - Alignment Length 101
 - Location of Alignment in SEQ ID NO 1966: from 1 to 67
 - Alignment No. 13718
 - gi No. 1942055
 - % Identity 77
 - Alignment Length 100
 - Location of Alignment in SEQ ID NO 1966: from 1 to 67

- Alignment No. 13719
- gi No. 2262173
- % Identity 72.3
- Alignment Length 101
- Location of Alignment in SEQ ID NO 1966: from 1 to 67
- Alignment No. 13720
- gi No. 2500128
- % Identity 70.2
- Alignment Length 94
- Location of Alignment in SEQ ID NO 1966: from 1 to 63
- Alignment No. 13721
- gi No. 2500129
- % Identity 71
- Alignment Length 100
- Location of Alignment in SEQ ID NO 1966: from 1 to 67
- Alignment No. 13722
- qi No. 2500130
- % Identity 70.1
- Alignment Length 77
- Location of Alignment in SEQ ID NO 1966: from 1 to 67

- (A) Polynucleotide Sequence
 - Pat. Appln. SEQ ID NO 1967
 - Ceres seq_id 1501813
 - (B) Polypeptide Sequence
 - Pat. Appln. SEQ ID NO 1968
 - Ceres seq_id 1501814
 - Location of start within SEQ ID NO 1967: at 1 nt.
- - (D) Related Amino Acid Sequences
 - Alignment No. 13723
 - gi No. 3128181
 - % Identity 74.6
 - Alignment Length 59
 - Location of Alignment in SEQ ID NO 1968: from 42 to 100
 - (B) Polypeptide Sequence
 - Pat. Appln. SEQ ID NO 1969
 - Ceres seq_id 1501815
 - Location of start within SEQ ID NO 1967: at 3 nt.
- - (D) Related Amino Acid Sequences
 - (B) Polypeptide Sequence
 - Pat. Appln. SEQ ID NO 1970
 - Ceres seq id 1501816
 - Location of start within SEQ ID NO 1967: at 124 nt.
- - (D) Related Amino Acid Sequences
 - Alignment No. 13724
 - gi No. 3128181

- % Identity 74.6
- Alignment Length 59
- Location of Alignment in SEQ ID NO 1970: from 1 to 59

- (A) Polynucleotide Sequence
 - Pat. Appln. SEQ ID NO 1971
 - Ceres seq_id 1501824
 - (B) Polypeptide Sequence
 - Pat. Appln. SEQ ID NO 1972
 - Ceres seq id 1501825
 - Location of start within SEQ ID NO 1971: at 304 nt.
- - Alignment No. 13725
 - GDP dissociation inhibitor
 - Location within SEQ ID NO 1972: from 1 to 100 aa.
 - (D) Related Amino Acid Sequences
 - Alignment No. 13726
 - gi No. 2384758
 - % Identity 70.1
 - Alignment Length 127
 - Location of Alignment in SEQ ID NO 1972: from 1 to 100
 - Alignment No. 13727
 - gi No. 2384760
 - % Identity 70.9
 - Alignment Length 127
 - Location of Alignment in SEQ ID NO 1972: from 1 to 100
 - Alignment No. 13728
 - gi No. 2501850
 - % Identity 74.2
 - Alignment Length 120
 - Location of Alignment in SEQ ID NO 1972: from 1 to 100
 - (B) Polypeptide Sequence
 - Pat. Appln. SEQ ID NO 1973
 - Ceres seg_id 1501826
 - Location of start within SEQ ID NO 1971: at 319 nt.
- (C) Nomination and Annotation of Domains within Predicted Polypeptide(s) $\label{eq:continuous} % \begin{array}{c} \text{Polypertide}(s) \\ \text{Polypertide}(s) \\ \end{array}$
 - Alignment No. 13729
 - GDP dissociation inhibitor
 - Location within SEQ ID NO 1973: from 1 to 95 aa.
 - (D) Related Amino Acid Sequences
 - Alignment No. 13730
 - gi No. 2384758
 - % Identity 70.1
 - Alignment Length 127
 - Location of Alignment in SEQ ID NO 1973: from 1 to 95
 - Alignment No. 13731
 - gi No. 2384760
 - % Identity 70.9
 - Alignment Length 127
 - Location of Alignment in SEQ ID NO 1973: from 1 to 95

- Alignment No. 13732
- gi No. 2501850
- % Identity 74.2
- Alignment Length 120
- Location of Alignment in SEQ ID NO 1973: from 1 to 95
- (B) Polypeptide Sequence
 - Pat. Appln. SEQ ID NO 1974
 - Ceres seq_id 1501827
 - Location of start within SEQ ID NO 1971: at 322 nt.
- - Alignment No. 13733
 - GDP dissociation inhibitor
 - Location within SEQ ID NO 1974: from 1 to 94 aa.
 - (D) Related Amino Acid Sequences
 - Alignment No. 13734
 - gi No. 2384758
 - % Identity 70.1
 - Alignment Length 127
 - Location of Alignment in SEQ ID NO 1974: from 1 to 94
 - Alignment No. 13735
 - gi No. 2384760
 - % Identity 70.9
 - Alignment Length 127
 - Location of Alignment in SEQ ID NO 1974: from 1 to 94
 - Alignment No. 13736
 - gi No. 2501850
 - % Identity 74.2
 - Alignment Length 120
 - Location of Alignment in SEQ ID NO 1974: from 1 to 94

- (A) Polynucleotide Sequence
 - Pat. Appln. SEQ ID NO 1975
 - Ceres seq_id 1501828
 - (B) Polypeptide Sequence
 - Pat. Appln. SEQ ID NO 1976
 - Ceres seq_id 1501829
 - Location of start within SEQ ID NO 1975: at 3 nt.
- (C) Nomination and Annotation of Domains within Predicted Polypeptide(s)
 - (D) Related Amino Acid Sequences
 - Alignment No. 13737
 - gi No. 3860272
 - % Identity 85.6
 - Alignment Length 105
 - Location of Alignment in SEQ ID NO 1976: from 62 to 163
 - (B) Polypeptide Sequence
 - Pat. Appln. SEQ ID NO 1977
 - Ceres seq id 1501830
 - Location of start within SEQ ID NO 1975: at 186 nt.

(C) Nomination and Annotation of Domains within Predicted

- (D) Related Amino Acid Sequences
 - Alignment No. 13738
 - gi No. 3860272
 - % Identity 85.6
 - Alignment Length 105
 - Location of Alignment in SEQ ID NO 1977: from 1 to 102

Maximum Length Sequence corresponding to clone ID 291908

(A) Polynucleotide Sequence

Polypeptide(s)

- Pat. Appln. SEQ ID NO 1978
- Ceres seq_id 1501850
- (B) Polypeptide Sequence
 - Pat. Appln. SEQ ID NO 1979
 - Ceres seq_id 1501851
 - Location of start within SEQ ID NO 1978: at 3 nt.
- (C) Nomination and Annotation of Domains within Predicted Polypeptide(s)
 - (D) Related Amino Acid Sequences
 - (B) Polypeptide Sequence
 - Pat. Appln. SEQ ID NO 1980
 - Ceres seq_id 1501852
 - Location of start within SEQ ID NO 1978: at 12 nt.
- (C) Nomination and Annotation of Domains within Predicted Polypeptide(s)
 - (D) Related Amino Acid Sequences
 - (B) Polypeptide Sequence
 - Pat. Appln. SEQ ID NO 1981
 - Ceres seq_id 1501853
 - Location of start within SEQ ID NO 1978: at 101 nt.
- - Alignment No. 13739
 - Thioredoxin
 - Location within SEQ ID NO 1981: from 31 to 139 aa.
 - (D) Related Amino Acid Sequences
 - Alignment No. 13740
 - gi No. 1848212
 - % Identity 75.4
 - Alignment Length 138
 - Location of Alignment in SEQ ID NO 1981: from 7 to 143
 - Alignment No. 13741
 - gi No. 2529680
 - % Identity 74.6
 - Alignment Length 138
 - Location of Alignment in SEQ ID NO 1981: from 7 to 143
 - Alignment No. 13742
 - gi No. 729442
 - % Identity 74.3
 - Alignment Length 140
 - Location of Alignment in SEQ ID NO 1981: from 5 to 143

- Alignment No. 13743
- gi No. 99991
- % Identity 89.5
- Alignment Length 19
- Location of Alignment in SEQ ID NO 1981: from 52 to 70
- Alignment No. 13744
- gi No. 99991
- % Identity 100
- Alignment Length 20
- Location of Alignment in SEQ ID NO 1981: from 51 to 70

- (A) Polynucleotide Sequence
 - Pat. Appln. SEQ ID NO 1982
 - Ceres seq id 1501862
 - (B) Polypeptide Sequence
 - Pat. Appln. SEQ ID NO 1983
 - Ceres seq_id 1501863
 - Location of start within SEQ ID NO 1982: at 3 nt.
- (C) Nomination and Annotation of Domains within Predicted Polypeptide(s)
 - (D) Related Amino Acid Sequences
 - (B) Polypeptide Sequence
 - Pat. Appln. SEQ ID NO 1984
 - Ceres seq_id 1501864
 - Location of start within SEQ ID NO 1982: at 76 nt.
- - Alignment No. 13745
 - Ribosomal protein L13e
 - Location within SEQ ID NO 1984: from 6 to 82 aa.
 - Alignment No. 13746
 - Fatty acid desaturase
 - Location within SEQ ID NO 1984: from 77 to 131 aa.
 - (D) Related Amino Acid Sequences
 - Alignment No. 13747
 - gi No. 1350664
 - % Identity 89
 - Alignment Length 73
 - Location of Alignment in SEQ ID NO 1984: from 10 to 82
 - Alignment No. 13748
 - gi No. 2662188
 - % Identity 70.6
 - Alignment Length 85
 - Location of Alignment in SEQ ID NO 1984: from 1 to 84
 - Alignment No. 13749
 - gi No. 730449
 - % Identity 86.9
 - Alignment Length 84
 - Location of Alignment in SEQ ID NO 1984: from 2 to 84
 - Alignment No. 13750
 - qi No. 730450

- % Identity 88.9
- Alignment Length 81
- Location of Alignment in SEQ ID NO 1984: from 2 to 82
- Alignment No. 13751
- qi No. 730526
- % Identity 88.9
- Alignment Length 81
- Location of Alignment in SEQ ID NO 1984: from 2 to 82
- (B) Polypeptide Sequence
 - Pat. Appln. SEQ ID NO 1985
 - Ceres seq_id 1501865
 - Location of start within SEQ ID NO 1982: at 274 nt.
- (C) Nomination and Annotation of Domains within Predicted Polypeptide(s)
 - Alignment No. 13752
 - Fatty acid desaturase
 - Location within SEQ ID NO 1985: from 11 to 65 aa.
 - (D) Related Amino Acid Sequences
 - Alignment No. 13753
 - gi No. 1350664
 - % Identity 89
 - Alignment Length 73
 - Location of Alignment in SEQ ID NO 1985: from 1 to 16
 - Alignment No. 13754
 - gi No. 2662188
 - % Identity 70.6
 - Alignment Length 85
 - Location of Alignment in SEQ ID NO 1985: from 1 to 18
 - Alignment No. 13755
 - gi No. 730449
 - % Identity 86.9
 - Alignment Length 84
 - Location of Alignment in SEQ ID NO 1985: from 1 to 18
 - Alignment No. 13756
 - gi No. 730450
 - % Identity 88.9
 - Alignment Length 81
 - Location of Alignment in SEQ ID NO 1985: from 1 to 16 $\,$
 - Alignment No. 13757
 - gi No. 730526
 - % Identity 88.9
 - Alignment Length 81
 - Location of Alignment in SEQ ID NO 1985: from 1 to 16

- (A) Polynucleotide Sequence
 - Pat. Appln. SEQ ID NO 1986
 - Ceres seq_id 1501872
 - (B) Polypeptide Sequence
 - Pat. Appln. SEQ ID NO 1987
 - Ceres seq_id 1501873
 - Location of start within SEQ ID NO 1986: at 3 nt.

- (C) Nomination and Annotation of Domains within Predicted Polypeptide(s)
 - (D) Related Amino Acid Sequences
 - (B) Polypeptide Sequence
 - Pat. Appln. SEQ ID NO 1988
 - Ceres seq_id 1501874
 - Location of start within SEQ ID NO 1986: at 92 nt.
- - Alignment No. 13758
 - Oleosin
 - Location within SEQ ID NO 1988: from 1 to 78 aa.
 - (D) Related Amino Acid Sequences
 - (B) Polypeptide Sequence
 - Pat. Appln. SEQ ID NO 1989
 - Ceres seq_id 1501875
 - Location of start within SEQ ID NO 1986: at 161 nt.
- (C) Nomination and Annotation of Domains within Predicted Polypeptide(s)
 - Alignment No. 13759
 - Oleosin
 - Location within SEQ ID NO 1989: from 1 to 55 aa.
 - (D) Related Amino Acid Sequences

- (A) Polynucleotide Sequence
 - Pat. Appln. SEQ ID NO 1990
 - Ceres seq_id 1501884
 - (B) Polypeptide Sequence
 - Pat. Appln. SEQ ID NO 1991
 - Ceres seq_id 1501885
 - Location of start within SEQ ID NO 1990: at 3 nt.
- (C) Nomination and Annotation of Domains within Predicted Polypeptide(s) $% \left(\frac{1}{2}\right) =\frac{1}{2}\left(\frac{1}{2}\right) +\frac{1}{2}\left(\frac{1}{2}\right) +\frac{$
 - (D) Related Amino Acid Sequences
 - (B) Polypeptide Sequence
 - Pat. Appln. SEQ ID NO 1992
 - Ceres seq id 1501886
 - Location of start within SEQ ID NO 1990: at 217 nt.
- (C) Nomination and Annotation of Domains within Predicted Polypeptide(s) $\label{eq:condition} % \begin{array}{c} \text{Polyperiod} \\ \text{Poly$
 - (D) Related Amino Acid Sequences
 - Alignment No. 13760
 - gi No. 166410
 - % Identity 78.8
 - Alignment Length 113
 - Location of Alignment in SEQ ID NO 1992: from 1 to 112
 - Alignment No. 13761
 - gi No. 3894178
 - % Identity 81.4
 - Alignment Length 102

- Location of Alignment in SEQ ID NO 1992: from 12 to 112
- Alignment No. 13762
- gi No. 4091080
- % Identity 79.3
- Alignment Length 111
- Location of Alignment in SEQ ID NO 1992: from 3 to 112
- Alignment No. 13763
- gi No. 4091117
- % Identity 79.3
- Alignment Length 111
- Location of Alignment in SEQ ID NO 1992: from 3 to 112
- Alignment No. 13764
- gi No. 4884860
- % Identity 75.7
- Alignment Length 115
- Location of Alignment in SEQ ID NO 1992: from 3 to 112
- (B) Polypeptide Sequence
 - Pat. Appln. SEQ ID NO 1993
 - Ceres seq_id 1501887
 - Location of start within SEQ ID NO 1990: at 346 nt.
- (C) Nomination and Annotation of Domains within Predicted Polypeptide(s)
 - (D) Related Amino Acid Sequences
 - Alignment No. 13765
 - gi No. 166410
 - % Identity 78.8
 - Alignment Length 113
 - Location of Alignment in SEQ ID NO 1993: from 1 to 69
 - Alignment No. 13766
 - gi No. 3894178
 - % Identity 81.4
 - Alignment Length 102
 - Location of Alignment in SEQ ID NO 1993: from 1 to 69
 - Alignment No. 13767
 - gi No. 4091080
 - % Identity 79.3
 - Alignment Length 111
 - Location of Alignment in SEQ ID NO 1993: from 1 to 69
 - Alignment No. 13768
 - qi No. 4091117
 - % Identity 79.3
 - Alignment Length 111
 - Location of Alignment in SEQ ID NO 1993: from 1 to 69
 - Alignment No. 13769
 - gi No. 4884860
 - % Identity 75.7
 - Alignment Length 115
 - Location of Alignment in SEQ ID NO 1993: from 1 to 69

- (A) Polynucleotide Sequence
 - Pat. Appln. SEQ ID NO 1994

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- Ceres seq_id 1501888
- (B) Polypeptide Sequence
 - Pat. Appln. SEQ ID NO 1995
 - Ceres seq id 1501889
 - Location of start within SEQ ID NO 1994: at 203 nt.
- (C) Nomination and Annotation of Domains within Predicted Polypeptide(s)
 - Alignment No. 13770
 - Aminotransferases class-I
 - Location within SEQ ID NO 1995: from 16 to 109 aa.
 - (D) Related Amino Acid Sequences
 - (B) Polypeptide Sequence
 - Pat. Appln. SEQ ID NO 1996
 - Ceres seq_id 1501890
 - Location of start within SEQ ID NO 1994: at 257 nt.
- (C) Nomination and Annotation of Domains within Predicted Polypeptide(s)
 - Alignment No. 13771
 - Aminotransferases class-I
 - Location within SEQ ID NO 1996: from 1 to 91 aa.
 - (D) Related Amino Acid Sequences
 - (B) Polypeptide Sequence
 - Pat. Appln. SEQ ID NO 1997
 - Ceres seg id 1501891
 - Location of start within SEQ ID NO 1994: at 299 nt.
- - Alignment No. 13772
 - Aminotransferases class-I
 - Location within SEQ ID NO 1997: from 1 to 77 aa.
 - (D) Related Amino Acid Sequences

- (A) Polynucleotide Sequence
 - Pat. Appln. SEQ ID NO 1998
 - Ceres seq_id 1501895
 - (B) Polypeptide Sequence
 - Pat. Appln. SEQ ID NO 1999
 - Ceres seq_id 1501896
 - Location of start within SEQ ID NO 1998: at 2 nt.
- - Alignment No. 13773
 - DnaJ domain
 - Location within SEQ ID NO 1999: from 5 to 51 aa.
 - (D) Related Amino Acid Sequences
 - Alignment No. 13774
 - gi No. 126757
 - % Identity 71.4
 - Alignment Length 35
 - Location of Alignment in SEQ ID NO 1999: from 13 to 47

- Alignment No. 13775
- gi No. 30851
- % Identity 70.8
- Alignment Length 24
- Location of Alignment in SEQ ID NO 1999: from 24 to 47
- (B) Polypeptide Sequence
 - Pat. Appln. SEQ ID NO 2000
 - Ceres seq id 1501897
 - Location of start within SEQ ID NO 1998: at 29 nt.
- - (D) Related Amino Acid Sequences
 - Alignment No. 13776
 - gi No. 126757
 - % Identity 71.4
 - Alignment Length 35
 - Location of Alignment in SEQ ID NO 2000: from 4 to 38
 - Alignment No. 13777
 - gi No. 30851
 - % Identity 70.8
 - Alignment Length 24
 - Location of Alignment in SEQ ID NO 2000: from 15 to 38
 - (B) Polypeptide Sequence
 - Pat. Appln. SEQ ID NO 2001
 - Ceres seq_id 1501898
 - Location of start within SEQ ID NO 1998: at 86 nt.
- - (D) Related Amino Acid Sequences
 - Alignment No. 13778
 - gi No. 126757
 - % Identity 71.4
 - Alignment Length 35
 - Location of Alignment in SEQ ID NO 2001: from 1 to 19
 - Alignment No. 13779
 - gi No. 30851
 - % Identity 70.8
 - Alignment Length 24
 - Location of Alignment in SEQ ID NO 2001: from 1 to 19

- (A) Polynucleotide Sequence
 - Pat. Appln. SEQ ID NO 2002
 - Ceres seq_id 1501899
 - (B) Polypeptide Sequence
 - Pat. Appln. SEQ ID NO 2003
 - Ceres seq id 1501900
 - Location of start within SEQ ID NO 2002: at 1 nt.
- (C) Nomination and Annotation of Domains within Predicted Polypeptide(s) $% \left(\frac{1}{2}\right) =\frac{1}{2}\left(\frac{1}{2}\right) +\frac{1}{2}\left(\frac{1}{2}\right) +\frac{$
 - Alignment No. 13780
 - Pyruvate kinase
 - Location within SEQ ID NO 2003: from 110 to 143 aa.

- (D) Related Amino Acid Sequences
 - Alignment No. 13781
 - gi No. 125606
 - % Identity 90
 - Alignment Length 40
 - Location of Alignment in SEQ ID NO 2003: from 105 to 143
 - Alignment No. 13782
 - gi No. 2497538
 - % Identity 87.5
 - Alignment Length 40
 - Location of Alignment in SEQ ID NO 2003: from 105 to 143
 - Alignment No. 13783
 - gi No. 2497543
 - % Identity 91.7
 - Alignment Length 36
 - Location of Alignment in SEQ ID NO 2003: from 109 to 143
 - Alignment No. 13784
 - gi No. 322787
 - % Identity 90
 - Alignment Length 40
 - Location of Alignment in SEQ ID NO 2003: from 105 to 143
 - Alignment No. 13785
 - gi No. 4033431
 - % Identity 86.1
 - Alignment Length 36
 - Location of Alignment in SEQ ID NO 2003: from 109 to 143
- (B) Polypeptide Sequence
 - Pat. Appln. SEQ ID NO 2004
 - Ceres seq_id 1501901
 - Location of start within SEQ ID NO 2002: at 3 nt.
- (C) Nomination and Annotation of Domains within Predicted Polypeptide(s) $% \left(\frac{1}{2}\right) =\frac{1}{2}\left(\frac{1}{2}\right) +\frac{1}{2}\left(\frac{1}{2}\right) +\frac{$
 - (D) Related Amino Acid Sequences
 - Alignment No. 13786
 - gi No. 2134206
 - % Identity 72.7
 - Alignment Length 11
 - Location of Alignment in SEQ ID NO 2004: from 53 to 63

- (A) Polynucleotide Sequence
 - Pat. Appln. SEQ ID NO 2005
 - Ceres seq id 1501902
 - (B) Polypeptide Sequence
 - Pat. Appln. SEQ ID NO 2006
 - Ceres seq_id 1501903
 - Location of start within SEQ ID NO 2005: at 1 nt.
- (C) Nomination and Annotation of Domains within Predicted Polypeptide(s) $\label{eq:condition} % \begin{array}{c} \text{Polyperiod} \\ \text{Poly$
 - (D) Related Amino Acid Sequences
 - Alignment No. 13787
 - gi No. 1947160
 - % Identity 72.7

- Alignment Length 11
- Location of Alignment in SEQ ID NO 2006: from 24 to 34
- Alignment No. 13788
- gi No. 3858883
- % Identity 72.7
- Alignment Length 11
- Location of Alignment in SEQ ID NO 2006: from 18 to 28
- Alignment No. 13789
- gi No. 4996894
- % Identity 72.7
- Alignment Length 11
- Location of Alignment in SEQ ID NO 2006: from 24 to 34
- (B) Polypeptide Sequence
 - Pat. Appln. SEQ ID NO 2007
 - Ceres seq_id 1501904
 - Location of start within SEQ ID NO 2005: at 2 nt.
- (C) Nomination and Annotation of Domains within Predicted Polypeptide(s)
 - Alignment No. 13790
 - Syndecan domain
 - Location within SEQ ID NO 2007: from 39 to 141 aa.
 - Alignment No. 13791
 - Assemblin (Peptidase family S21)
 - Location within SEQ ID NO 2007: from 24 to 139 aa.
 - Alignment No. 13792
 - Mucin-like glycoprotein
 - Location within SEQ ID NO 2007: from 35 to 140 aa.
 - Alignment No. 13793
 - Mucin-like glycoprotein
 - Location within SEQ ID NO 2007: from 35 to 141 aa.
 - Alignment No. 13794
 - Mucin-like glycoprotein
 - Location within SEQ ID NO 2007: from 41 to 139 aa.
 - Alignment No. 13795
 - Mucin-like glycoprotein
 - Location within SEQ ID NO 2007: from 59 to 139 aa.
 - Alignment No. 13796
 - Mucin-like glycoprotein
 - Location within SEQ ID NO 2007: from 76 to 139 aa.
 - Alignment No. 13797
 - 7 transmembrane receptor (rhodopsin family)
 - Location within SEQ ID NO 2007: from 21 to 137 aa.
 - Alignment No. 13798
 - 7 transmembrane receptor (rhodopsin family)
 - Location within SEQ ID NO 2007: from 21 to 141 aa.
 - (D) Related Amino Acid Sequences
 - Alignment No. 13799
 - gi No. 585527

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- % Identity 71.4
- Alignment Length 14
- Location of Alignment in SEQ ID NO 2007: from 128 to 141
- (B) Polypeptide Sequence
 - Pat. Appln. SEQ ID NO 2008
 - Ceres seg id 1501905
 - Location of start within SEQ ID NO 2005: at 3 nt.
- (C) Nomination and Annotation of Domains within Predicted Polypeptide(s) $\label{eq:continuous}$
 - (D) Related Amino Acid Sequences
 - Alignment No. 13800
 - gi No. 113928
 - % Identity 75
 - Alignment Length 12
 - Location of Alignment in SEQ ID NO 2008: from 7 to 18
 - Alignment No. 13801
 - gi No. 1914853
 - % Identity 72.7
 - Alignment Length 11
 - Location of Alignment in SEQ ID NO 2008: from 18 to 28
 - Alignment No. 13802
 - gi No. 2077900
 - % Identity 72.7
 - Alignment Length 11
 - Location of Alignment in SEQ ID NO 2008: from 17 to 27
 - Alignment No. 13803
 - gi No. 280655
 - % Identity 75
 - Alignment Length 12
 - Location of Alignment in SEQ ID NO 2008: from 7 to 18

- (A) Polynucleotide Sequence
 - Pat. Appln. SEQ ID NO 2009
 - Ceres seq_id 1501906
 - (B) Polypeptide Sequence
 - Pat. Appln. SEQ ID NO 2010
 - Ceres seq_id 1501907
 - Location of start within SEQ ID NO 2009: at 2 nt.
- (C) Nomination and Annotation of Domains within Predicted Polypeptide(s) $\label{eq:condition}$
 - (D) Related Amino Acid Sequences
 - Alignment No. 13804
 - qi No. 2909522
 - % Identity 75
 - Alignment Length 28
 - Location of Alignment in SEQ ID NO 2010: from 1 to 28
 - (B) Polypeptide Sequence
 - Pat. Appln. SEQ ID NO 2011
 - Ceres seq_id 1501908
 - Location of start within SEQ ID NO 2009: at 388 nt.
- (C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

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- (D) Related Amino Acid Sequences
- (B) Polypeptide Sequence
 - Pat. Appln. SEQ ID NO 2012
 - Ceres seq id 1501909
 - Location of start within SEQ ID NO 2009: at 407 nt.
- - (D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 293854

- (A) Polynucleotide Sequence
 - Pat. Appln. SEQ ID NO 2013
 - Ceres seq_id 1501922
 - (B) Polypeptide Sequence
 - Pat. Appln. SEQ ID NO 2014
 - Ceres seq_id 1501923
 - Location of start within SEQ ID NO 2013: at 208 nt.
- - Alignment No. 13805
 - Peroxidase
 - Location within SEQ ID NO 2014: from 48 to 113 aa.
 - (D) Related Amino Acid Sequences
 - (B) Polypeptide Sequence
 - Pat. Appln. SEQ ID NO 2015
 - Ceres seq_id 1501924
 - Location of start within SEQ ID NO 2013: at 223 nt.
- (C) Nomination and Annotation of Domains within Predicted Polypeptide(s)
 - Alignment No. 13806
 - Peroxidase
 - Location within SEQ ID NO 2015: from 43 to 108 aa.
 - (D) Related Amino Acid Sequences
 - (B) Polypeptide Sequence
 - Pat. Appln. SEQ ID NO 2016
 - Ceres seq_id 1501925
 - Location of start within SEQ ID NO 2013: at 226 nt.
- - Alignment No. 13807
 - Peroxidase
 - Location within SEQ ID NO 2016: from 42 to 107 aa.
 - (D) Related Amino Acid Sequences

- (A) Polynucleotide Sequence
 - Pat. Appln. SEQ ID NO 2017
 - Ceres seq_id 1501926
 - (B) Polypeptide Sequence
 - Pat. Appln. SEQ ID NO 2018
 - Ceres seq_id 1501927

- Location of start within SEQ ID NO 2017: at 190 nt.
- (C) Nomination and Annotation of Domains within Predicted Polypeptide(s)
 - Alignment No. 13808
 - Synaptobrevin
 - Location within SEQ ID NO 2018: from 62 to 121 aa.
 - (D) Related Amino Acid Sequences
 - Alignment No. 13809
 - gi No. 3157951
 - % Identity 88.5
 - Alignment Length 61
 - Location of Alignment in SEQ ID NO 2018: from 62 to 121
 - (B) Polypeptide Sequence
 - Pat. Appln. SEQ ID NO 2019
 - Ceres seq id 1501928
 - Location of start within SEQ ID NO 2017: at 205 nt.
- (C) Nomination and Annotation of Domains within Predicted Polypeptide(s) $% \left(\frac{1}{2}\right) =\frac{1}{2}\left(\frac{1}{2}\right) +\frac{1}{2}\left(\frac{1}{2}\right) +\frac{$
 - Alignment No. 13810
 - Synaptobrevin
 - Location within SEQ ID NO 2019: from 57 to 116 aa.
 - (D) Related Amino Acid Sequences
 - Alignment No. 13811
 - gi No. 3157951
 - % Identity 88.5
 - Alignment Length 61
 - Location of Alignment in SEQ ID NO 2019: from 57 to 116
 - (B) Polypeptide Sequence
 - Pat. Appln. SEQ ID NO 2020
 - Ceres seq_id 1501929
 - Location of start within SEQ ID NO 2017: at 346 nt.
- (C) Nomination and Annotation of Domains within Predicted Polypeptide(s) $% \left(\frac{1}{2}\right) =\frac{1}{2}\left(\frac{1}{2}\right) +\frac{1}{2}\left(\frac{1}{2}\right) +\frac{$
 - Alignment No. 13812
 - Synaptobrevin
 - Location within SEQ ID NO 2020: from 10 to 69 aa.
 - (D) Related Amino Acid Sequences
 - Alignment No. 13813
 - gi No. 3157951
 - % Identity 88.5
 - Alignment Length 61
 - Location of Alignment in SEQ ID NO 2020: from 10 to 69

- (A) Polynucleotide Sequence
 - Pat. Appln. SEQ ID NO 2021
 - Ceres seq id 1501930
 - (B) Polypeptide Sequence
 - Pat. Appln. SEQ ID NO 2022
 - Ceres seq id 1501931
 - Location of start within SEQ ID NO 2021: at 2 nt.

- - (D) Related Amino Acid Sequences
 - (B) Polypeptide Sequence
 - Pat. Appln. SEQ ID NO 2023
 - Ceres seq id 1501932
 - Location of start within SEQ ID NO 2021: at 97 nt.
- - (D) Related Amino Acid Sequences
 - Alignment No. 13814
 - gi No. 2213626
 - % Identity 73.7
 - Alignment Length 19
 - Location of Alignment in SEQ ID NO 2023: from 9 to 27
 - Alignment No. 13815
 - gi No. 4850408
 - % Identity 73.7
 - Alignment Length 19
 - Location of Alignment in SEQ ID NO 2023: from 13 to 31
 - (B) Polypeptide Sequence
 - Pat. Appln. SEQ ID NO 2024
 - Ceres seq_id 1501933
 - Location of start within SEQ ID NO 2021: at 240 nt.
- - (D) Related Amino Acid Sequences

 ${\tt Maximum\ Length\ Sequence\ corresponding\ to\ clone\ ID\ 293882}$

- (A) Polynucleotide Sequence
 - Pat. Appln. SEQ ID NO 2025
 - Ceres seq_id 1501949
 - (B) Polypeptide Sequence
 - Pat. Appln. SEQ ID NO 2026
 - Ceres seq_id 1501950
 - Location of start within SEO ID NO 2025: at 1 nt.
- (C) Nomination and Annotation of Domains within Predicted Polypeptide(s)
 - (D) Related Amino Acid Sequences
 - (B) Polypeptide Sequence
 - Pat. Appln. SEQ ID NO 2027
 - Ceres seq_id 1501951
 - Location of start within SEQ ID NO 2025: at 2 nt.
- (C) Nomination and Annotation of Domains within Predicted Polypeptide(s)
 - (D) Related Amino Acid Sequences
 - (B) Polypeptide Sequence
 - Pat. Appln. SEQ ID NO 2028
 - Ceres seq_id 1501952
 - Location of start within SEQ ID NO 2025: at 96 nt.

- - Alignment No. 13816
 - ABC transporter
 - Location within SEQ ID NO 2028: from 83 to 147 aa.
 - (D) Related Amino Acid Sequences

- (A) Polynucleotide Sequence
 - Pat. Appln. SEQ ID NO 2029
 - Ceres seq_id 1501976
 - (B) Polypeptide Sequence
 - Pat. Appln. SEQ ID NO 2030
 - Ceres seq id 1501977
 - Location of start within SEQ ID NO 2029: at 2 nt.
- (C) Nomination and Annotation of Domains within Predicted Polypeptide(s) $% \left(\frac{1}{2}\right) =\frac{1}{2}\left(\frac{1}{2}\right) +\frac{1}{2}\left(\frac{1}{2}\right) +\frac{$
 - (D) Related Amino Acid Sequences
 - (B) Polypeptide Sequence
 - Pat. Appln. SEQ ID NO 2031
 - Ceres seq id 1501978
 - Location of start within SEQ ID NO 2029: at 3 nt.
- (C) Nomination and Annotation of Domains within Predicted Polypeptide(s) $% \left(\frac{1}{2}\right) =\frac{1}{2}\left(\frac{1}{2}\right) +\frac{1}{2}\left(\frac{1}{2}\right) +\frac{$
 - (D) Related Amino Acid Sequences
 - Alignment No. 13817
 - gi No. 4678325
 - % Identity 78.6
 - Alignment Length 70
 - Location of Alignment in SEQ ID NO 2031: from 41 to 110
 - (B) Polypeptide Sequence
 - Pat. Appln. SEQ ID NO 2032
 - Ceres seq_id 1501979
 - Location of start within SEQ ID NO 2029: at 75 nt.
- (C) Nomination and Annotation of Domains within Predicted Polypeptide(s)
 - (D) Related Amino Acid Sequences
 - Alignment No. 13818
 - gi No. 4678325
 - % Identity 78.6
 - Alignment Length 70
 - Location of Alignment in SEQ ID NO 2032: from 17 to 86

- (A) Polynucleotide Sequence
 - Pat. Appln. SEQ ID NO 2033
 - Ceres seq_id 1502003
 - (B) Polypeptide Sequence
 - Pat. Appln. SEQ ID NO 2034
 - Ceres seq_id 1502004
 - Location of start within SEQ ID NO 2033: at 2 nt.
- (C) Nomination and Annotation of Domains within Predicted Polypeptide(s) $\label{eq:condition} % \begin{array}{c} \text{Polyperiod} \\ \text{Poly$
 - (D) Related Amino Acid Sequences

- (B) Polypeptide Sequence
 - Pat. Appln. SEQ ID NO 2035
 - Ceres seq_id 1502005
 - Location of start within SEQ ID NO 2033: at 3 nt.
- - Alignment No. 13819
 - Gag polyprotein, inner coat protein p12
 - Location within SEQ ID NO 2035: from 35 to 89 aa.
 - Alignment No. 13820
 - Mucin-like glycoprotein
 - Location within SEQ ID NO 2035: from 12 to 130 aa.
 - Alignment No. 13821
 - 7 transmembrane receptor (rhodopsin family)
 - Location within SEQ ID NO 2035: from 27 to 85 aa.
 - Alignment No. 13822
 - 7 transmembrane receptor (rhodopsin family)
 - Location within SEQ ID NO 2035: from 27 to 93 aa.
 - Alignment No. 13823
 - 7 transmembrane receptor (rhodopsin family)
 - Location within SEQ ID NO 2035: from 33 to 116 aa.
 - Alignment No. 13824
 - 7 transmembrane receptor (rhodopsin family)
 - Location within SEQ ID NO 2035: from 34 to 116 aa.
 - (D) Related Amino Acid Sequences
 - Alignment No. 13825
 - gi No. 2134206
 - % Identity 72.7
 - Alignment Length 11
 - Location of Alignment in SEQ ID NO 2035: from 136 to 146
 - Alignment No. 13826
 - gi No. 2134208
 - % Identity 72.7
 - Alignment Length 11
 - Location of Alignment in SEQ ID NO 2035: from 136 to 146
 - Alignment No. 13827
 - gi No. 2134209
 - % Identity 72.7
 - Alignment Length 11
 - Location of Alignment in SEQ ID NO 2035: from 136 to 146
 - Alignment No. 13828
 - gi No. 2507155
 - % Identity 72.7
 - Alignment Length 11
 - Location of Alignment in SEQ ID NO 2035: from 45 to 55
 - Alignment No. 13829
 - qi No. 439289
 - % Identity 72.7
 - Alignment Length 11

- Location of Alignment in SEQ ID NO 2035: from 45 to 55
- Alignment No. 13830
- gi No. 871535
- % Identity 72.7
- Alignment Length 11
- Location of Alignment in SEQ ID NO 2035: from 45 to 55
- Alignment No. 13831
- gi No. 93144
- % Identity 76.2
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2035: from 32 to 52
- Alignment No. 13832
- gi No. 93144
- % Identity 73.9
- Alignment Length 24
- Location of Alignment in SEQ ID NO 2035: from 32 to 54
- (B) Polypeptide Sequence
 - Pat. Appln. SEQ ID NO 2036
 - Ceres seq_id 1502006
 - Location of start within SEQ ID NO 2033: at 116 nt.
- (C) Nomination and Annotation of Domains within Predicted Polypeptide(s)
 - (D) Related Amino Acid Sequences

- (A) Polynucleotide Sequence
 - Pat. Appln. SEQ ID NO 2037
 - Ceres seq id 1502011
 - (B) Polypeptide Sequence
 - Pat. Appln. SEQ ID NO 2038
 - Ceres seq_id 1502012
 - Location of start within SEQ ID NO 2037: at 2 nt.
- (C) Nomination and Annotation of Domains within Predicted Polypeptide(s) $% \left(1\right) =\left(1\right) \left(1\right) +\left(1\right) \left(1\right) \left(1\right) +\left(1\right) \left(1\right)$
 - (D) Related Amino Acid Sequences
 - Alignment No. 13833
 - gi No. 3915131
 - % Identity 76.3
 - Alignment Length 38
 - Location of Alignment in SEQ ID NO 2038: from 24 to 61
 - (B) Polypeptide Sequence
 - Pat. Appln. SEQ ID NO 2039
 - Ceres seq id 1502013
 - Location of start within SEQ ID NO 2037: at 210 nt.
- (C) Nomination and Annotation of Domains within Predicted Polypeptide(s) $\label{eq:continuous} % \begin{array}{c} \text{Polyperiod} \\ \text{Pol$
 - Alignment No. 13834
 - GMC oxidoreductases
 - Location within SEQ ID NO 2039: from 1 to 55 aa.
 - (D) Related Amino Acid Sequences
 - Alignment No. 13835
 - gi No. 4903006

- % Identity 71.4
- Alignment Length 70
- Location of Alignment in SEQ ID NO 2039: from 1 to 63
- Alignment No. 13836
- gi No. 4903018
- % Identity 71.4
- Alignment Length 70
- Location of Alignment in SEQ ID NO 2039: from 1 to 63
- (B) Polypeptide Sequence
 - Pat. Appln. SEQ ID NO 2040
 - Ceres seq_id 1502014
 - Location of start within SEQ ID NO 2037: at 575 nt.
- (C) Nomination and Annotation of Domains within Predicted Polypeptide(s)
 - (D) Related Amino Acid Sequences

- (A) Polynucleotide Sequence
 - Pat. Appln. SEQ ID NO 2041
 - Ceres seq_id 1502015
 - (B) Polypeptide Sequence
 - Pat. Appln. SEQ ID NO 2042
 - Ceres seq_id 1502016
 - Location of start within SEQ ID NO 2041: at 2 nt.
- - (D) Related Amino Acid Sequences
 - (B) Polypeptide Sequence
 - Pat. Appln. SEQ ID NO 2043
 - Ceres seq_id 1502017
 - Location of start within SEQ ID NO 2041: at 3 nt.
- (C) Nomination and Annotation of Domains within Predicted Polypeptide(s) $% \left(\frac{1}{2}\right) =\frac{1}{2}\left(\frac{1}{2}\right) +\frac{1}{2}\left(\frac{1}{2}\right) +\frac{$
 - (D) Related Amino Acid Sequences
 - Alignment No. 13837
 - gi No. 82087
 - % Identity 71.4
 - Alignment Length 14
 - Location of Alignment in SEQ ID NO 2043: from 41 to 54
 - Alignment No. 13838
 - gi No. 82087
 - % Identity 71.4
 - Alignment Length 14
 - Location of Alignment in SEQ ID NO 2043: from 41 to 54
 - (B) Polypeptide Sequence
 - Pat. Appln. SEQ ID NO 2044
 - Ceres seq_id 1502018
 - Location of start within SEQ ID NO 2041: at 78 nt.
- - (D) Related Amino Acid Sequences
 - Alignment No. 13839

- gi No. 82087
- % Identity 71.4
- Alignment Length 14
- Location of Alignment in SEQ ID NO 2044: from 16 to 29
- Alignment No. 13840
- gi No. 82087
- % Identity 71.4
- Alignment Length 14
- Location of Alignment in SEQ ID NO 2044: from 16 to 29

- (A) Polynucleotide Sequence
 - Pat. Appln. SEQ ID NO 2045
 - Ceres seq_id 1502023
 - (B) Polypeptide Sequence
 - Pat. Appln. SEQ ID NO 2046
 - Ceres seq_id 1502024
 - Location of start within SEQ ID NO 2045: at 126 nt.
- - Alignment No. 13841
 - Zinc finger, C3HC4 type (RING finger)
 - Location within SEQ ID NO 2046: from 78 to 129 aa.
 - (D) Related Amino Acid Sequences
 - (B) Polypeptide Sequence
 - Pat. Appln. SEQ ID NO 2047
 - Ceres seq_id 1502025
 - Location of start within SEQ ID NO 2045: at 289 nt.
- - (D) Related Amino Acid Sequences
 - (B) Polypeptide Sequence
 - Pat. Appln. SEQ ID NO 2048
 - Ceres seq_id 1502026
 - Location of start within SEQ ID NO 2045: at 298 nt.
- - (D) Related Amino Acid Sequences

- (A) Polynucleotide Sequence
 - Pat. Appln. SEQ ID NO 2049
 - Ceres seq_id 1502027
 - (B) Polypeptide Sequence
 - Pat. Appln. SEQ ID NO 2050
 - Ceres seq_id 1502028
 - Location of start within SEQ ID NO 2049: at 2 nt.
- (C) Nomination and Annotation of Domains within Predicted Polypeptide(s)
 - (D) Related Amino Acid Sequences
 - (B) Polypeptide Sequence
 - Pat. Appln. SEQ ID NO 2051

- Ceres seq_id 1502029
- Location of start within SEQ ID NO 2049: at 3 nt.
- (C) Nomination and Annotation of Domains within Predicted Polypeptide(s)
 - (D) Related Amino Acid Sequences
 - (B) Polypeptide Sequence
 - Pat. Appln. SEQ ID NO 2052
 - Ceres seq_id 1502030
 - Location of start within SEQ ID NO 2049: at 256 nt.
- (C) Nomination and Annotation of Domains within Predicted Polypeptide(s)
 - Alignment No. 13842
 - Ubiquitin-conjugating enzyme
 - Location within SEQ ID NO 2052: from 1 to 81 aa.
 - (D) Related Amino Acid Sequences
 - Alignment No. 13843
 - gi No. 1174852
 - % Identity 78.9
 - Alignment Length 76
 - Location of Alignment in SEQ ID NO 2052: from 7 to 81
 - Alignment No. 13844
 - gi No. 136647
 - % Identity 86.7
 - Alignment Length 60
 - Location of Alignment in SEQ ID NO 2052: from 23 to 81
 - Alignment No. 13845
 - gi No. 2129758
 - % Identity 83.1
 - Alignment Length 77
 - Location of Alignment in SEQ ID NO 2052: from 6 to 81
 - Alignment No. 13846
 - gi No. 2624417
 - % Identity 98.8
 - Alignment Length 82
 - Location of Alignment in SEQ ID NO 2052: from 1 to 81
 - Alignment No. 13847
 - gi No. 2641619
 - % Identity 89
 - Alignment Length 82
 - Location of Alignment in SEQ ID NO 2052: from 1 to 81
 - Alignment No. 13848
 - gi No. 992706
 - % Identity 80.5
 - Alignment Length 77
 - Location of Alignment in SEQ ID NO 2052: from 6 to 81

- (A) Polynucleotide Sequence
 - Pat. Appln. SEQ ID NO 2053
 - Ceres seq_id 1502031
 - (B) Polypeptide Sequence
 - Pat. Appln. SEQ ID NO 2054

- Ceres seq_id 1502032
- Location of start within SEQ ID NO 2053: at 1 nt.
- - Alignment No. 13849
 - Aminotransferases class-III pyridoxal-phosphate
 - Location within SEQ ID NO 2054: from 110 to 174 aa.
 - (D) Related Amino Acid Sequences
 - Alignment No. 13850
 - gi No. 100332
 - % Identity 70.4
 - Alignment Length 142
 - Location of Alignment in SEQ ID NO 2054: from 35 to 174
 - Alignment No. 13851
 - gi No. 1170029
 - % Identity 85.7
 - Alignment Length 154
 - Location of Alignment in SEQ ID NO 2054: from 22 to 174
 - Alignment No. 13852
 - gi No. 1170031
 - % Identity 71.4
 - Alignment Length 148
 - Location of Alignment in SEQ ID NO 2054: from 29 to 174
 - Alignment No. 13853
 - gi No. 1170032
 - % Identity 74
 - Alignment Length 104
 - Location of Alignment in SEQ ID NO 2054: from 72 to 174
 - Alignment No. 13854
 - gi No. 2492858
 - % Identity 76.1
 - Alignment Length 92
 - Location of Alignment in SEQ ID NO 2054: from 84 to 174
 - Alignment No. 13855
 - gi No. 2492862
 - % Identity 77.2
 - Alignment Length 123
 - Location of Alignment in SEQ ID NO 2054: from 53 to 174
 - Alignment No. 13856
 - gi No. 2982001
 - % Identity 74
 - Alignment Length 104
 - Location of Alignment in SEQ ID NO 2054: from 72 to 174
 - Alignment No. 13857
 - gi No. 399785
 - % Identity 78
 - Alignment Length 123
 - Location of Alignment in SEQ ID NO 2054: from 53 to 174
 - Alignment No. 13858
 - gi No. 97570
 - % Identity 75

- Alignment Length 104
- Location of Alignment in SEQ ID NO 2054: from 72 to 174
- (B) Polypeptide Sequence
 - Pat. Appln. SEQ ID NO 2055
 - Ceres seq_id 1502033
 - Location of start within SEQ ID NO 2053: at 64 nt.
- (C) Nomination and Annotation of Domains within Predicted Polypeptide(s)
 - Alignment No. 13859
 - Aminotransferases class-III pyridoxal-phosphate
 - Location within SEQ ID NO 2055: from 89 to 153 aa.
 - (D) Related Amino Acid Sequences
 - Alignment No. 13860
 - gi No. 100332
 - % Identity 70.4
 - Alignment Length 142
 - Location of Alignment in SEQ ID NO 2055: from 14 to 153
 - Alignment No. 13861
 - gi No. 1170029
 - % Identity 85.7
 - Alignment Length 154
 - Location of Alignment in SEQ ID NO 2055: from 1 to 153
 - Alignment No. 13862
 - gi No. 1170031
 - % Identity 71.4
 - Alignment Length 148
 - Location of Alignment in SEQ ID NO 2055: from 8 to 153
 - Alignment No. 13863
 - gi No. 1170032
 - % Identity 74
 - Alignment Length 104
 - Location of Alignment in SEQ ID NO 2055: from 51 to 153
 - Alignment No. 13864
 - gi No. 2492858
 - % Identity 76.1
 - Alignment Length 92
 - Location of Alignment in SEQ ID NO 2055: from 63 to 153
 - Alignment No. 13865
 - gi No. 2492862
 - % Identity 77.2
 - Alignment Length 123
 - Location of Alignment in SEQ ID NO 2055: from 32 to 153
 - Alignment No. 13866
 - gi No. 2982001
 - % Identity 74
 - Alignment Length 104
 - Location of Alignment in SEQ ID NO 2055: from 51 to 153
 - Alignment No. 13867
 - gi No. 399785
 - % Identity 78
 - Alignment Length 123

- Location of Alignment in SEQ ID NO 2055: from 32 to 153
- Alignment No. 13868
- gi No. 97570
- % Identity 75
- Alignment Length 104
- Location of Alignment in SEQ ID NO 2055: from 51 to 153
- (B) Polypeptide Sequence
 - Pat. Appln. SEQ ID NO 2056
 - Ceres seq_id 1502034
 - Location of start within SEQ ID NO 2053: at 124 nt.
- - Alignment No. 13869
 - Aminotransferases class-III pyridoxal-phosphate
 - Location within SEQ ID NO 2056: from 69 to 133 aa.
 - (D) Related Amino Acid Sequences
 - Alignment No. 13870
 - gi No. 100332
 - % Identity 70.4
 - Alignment Length 142
 - Location of Alignment in SEQ ID NO 2056: from 1 to 133
 - Alignment No. 13871
 - gi No. 1170029
 - % Identity 85.7
 - Alignment Length 154
 - Location of Alignment in SEQ ID NO 2056: from 1 to 133
 - Alignment No. 13872
 - gi No. 1170031
 - % Identity 71.4
 - Alignment Length 148
 - Location of Alignment in SEQ ID NO 2056: from 1 to 133
 - Alignment No. 13873
 - gi No. 1170032
 - % Identity 74
 - Alignment Length 104
 - Location of Alignment in SEQ ID NO 2056: from 31 to 133
 - Alignment No. 13874
 - gi No. 2492858
 - % Identity 76.1
 - Alignment Length 92
 - Location of Alignment in SEQ ID NO 2056: from 43 to 133
 - Alignment No. 13875
 - qi No. 2492862
 - % Identity 77.2
 - Alignment Length 123
 - Location of Alignment in SEQ ID NO 2056: from 12 to 133
 - Alignment No. 13876
 - gi No. 2982001
 - % Identity 74
 - Alignment Length 104
 - Location of Alignment in SEQ ID NO 2056: from 31 to 133

- Alignment No. 13877
- gi No. 399785
- % Identity 78
- Alignment Length 123
- Location of Alignment in SEQ ID NO 2056: from 12 to 133
- Alignment No. 13878
- gi No. 97570
- % Identity 75
- Alignment Length 104
- Location of Alignment in SEQ ID NO 2056: from 31 to 133

- (A) Polynucleotide Sequence
 - Pat. Appln. SEQ ID NO 2057
 - Ceres seq_id 1502035
 - (B) Polypeptide Sequence
 - Pat. Appln. SEQ ID NO 2058
 - Ceres seq_id 1502036
 - Location of start within SEQ ID NO 2057: at 72 nt.
- (C) Nomination and Annotation of Domains within Predicted Polypeptide(s)
 - Alignment No. 13879
 - Bowman-Birk serine protease inhibitor family
 - Location within SEQ ID NO 2058: from 67 to 119 aa.
 - (D) Related Amino Acid Sequences
 - (B) Polypeptide Sequence
 - Pat. Appln. SEQ ID NO 2059
 - Ceres seq_id 1502037
 - Location of start within SEQ ID NO 2057: at 78 nt.
- - Alignment No. 13880
 - Bowman-Birk serine protease inhibitor family
 - Location within SEQ ID NO 2059: from 65 to 117 aa.
 - (D) Related Amino Acid Sequences
 - (B) Polypeptide Sequence
 - Pat. Appln. SEQ ID NO 2060
 - Ceres seq_id 1502038
 - Location of start within SEQ ID NO 2057: at 102 nt.
- - Alignment No. 13881
 - Bowman-Birk serine protease inhibitor family
 - Location within SEQ ID NO 2060: from 57 to 109 aa.
 - (D) Related Amino Acid Sequences

- (A) Polynucleotide Sequence
 - Pat. Appln. SEQ ID NO 2061
 - Ceres seq_id 1502048
 - (B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2062
- Ceres seq id 1502049
- Location of start within SEQ ID NO 2061: at 3 nt.
- (C) Nomination and Annotation of Domains within Predicted Polypeptide(s)
 - (D) Related Amino Acid Sequences
 - (B) Polypeptide Sequence
 - Pat. Appln. SEQ ID NO 2063
 - Ceres seq id 1502050
 - Location of start within SEQ ID NO 2061: at 109 nt.
- - Alignment No. 13882
 - Sugar (and other) transporter
 - Location within SEQ ID NO 2063: from 26 to 175 aa.
 - (D) Related Amino Acid Sequences

- (A) Polynucleotide Sequence
 - Pat. Appln. SEQ ID NO 2064
 - Ceres seq_id 1502056
 - (B) Polypeptide Sequence
 - Pat. Appln. SEQ ID NO 2065
 - Ceres seq_id 1502057
 - Location of start within SEQ ID NO 2064: at 1 nt.
- - (D) Related Amino Acid Sequences
 - (B) Polypeptide Sequence
 - Pat. Appln. SEQ ID NO 2066
 - Ceres seq_id 1502058
 - Location of start within SEQ ID NO 2064: at 330 nt.
- - (D) Related Amino Acid Sequences
 - Alignment No. 13883
 - gi No. 3402683
 - % Identity 81.5
 - Alignment Length 27
 - Location of Alignment in SEQ ID NO 2066: from 22 to 48
 - Alignment No. 13884
 - gi No. 4678298
 - % Identity 95.7
 - Alignment Length 23
 - Location of Alignment in SEQ ID NO 2066: from 22 to 44
 - Alignment No. 13885
 - qi No. 4914404
 - % Identity 79.3
 - Alignment Length 29
 - Location of Alignment in SEQ ID NO 2066: from 24 to 52
 - (B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2067
- Ceres seq id 1502059
- Location of start within SEQ ID NO 2064: at 348 nt.
- (C) Nomination and Annotation of Domains within Predicted Polypeptide(s) $% \left(\frac{1}{2}\right) =\frac{1}{2}\left(\frac{1}{2}\right) +\frac{1}{2}\left(\frac{1}{2}\right) +\frac{$
 - (D) Related Amino Acid Sequences
 - Alignment No. 13886
 - gi No. 3402683
 - % Identity 81.5
 - Alignment Length 27
 - Location of Alignment in SEQ ID NO 2067: from 16 to 42
 - Alignment No. 13887
 - gi No. 4678298
 - % Identity 95.7
 - Alignment Length 23
 - Location of Alignment in SEQ ID NO 2067: from 16 to 38
 - Alignment No. 13888
 - gi No. 4914404
 - % Identity 79.3
 - Alignment Length 29
 - Location of Alignment in SEQ ID NO 2067: from 18 to 46

- (A) Polynucleotide Sequence
 - Pat. Appln. SEQ ID NO 2068
 - Ceres seq_id 1502066
 - (B) Polypeptide Sequence
 - Pat. Appln. SEQ ID NO 2069
 - Ceres seq_id 1502067
 - Location of start within SEQ ID NO 2068: at 140 nt.
- - Alignment No. 13889
 - DnaJ domain
 - Location within SEQ ID NO 2069: from 12 to 79 aa.
 - (D) Related Amino Acid Sequences

- (A) Polynucleotide Sequence
 - Pat. Appln. SEQ ID NO 2070
 - Ceres seq_id 1502074
 - (B) Polypeptide Sequence
 - Pat. Appln. SEQ ID NO 2071
 - Ceres seq_id 1502075
 - Location of start within SEQ ID NO 2070: at 2 nt.
- (C) Nomination and Annotation of Domains within Predicted Polypeptide(s) $\label{eq:continuous}$
 - Alignment No. 13890
 - Collagen triple helix repeat (20 copies)
 - Location within SEQ ID NO 2071: from 70 to 120 aa.
 - Alignment No. 13891
 - Mucin-like glycoprotein
 - Location within SEQ ID NO 2071: from 34 to 153 aa.

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- Alignment No. 13892
- Mucin-like glycoprotein
- Location within SEQ ID NO 2071: from 58 to 148 aa.
- Alignment No. 13893
- Mucin-like glycoprotein
- Location within SEQ ID NO 2071: from 58 to 151 aa.
- Alignment No. 13894
- 7 transmembrane receptor (rhodopsin family)
- Location within SEQ ID NO 2071: from 41 to 153 aa.
- Alignment No. 13895
- 7 transmembrane receptor (rhodopsin family)
- Location within SEQ ID NO 2071: from 48 to 153 aa.
- Alignment No. 13896
- 7 transmembrane receptor (rhodopsin family)
- Location within SEQ ID NO 2071: from 59 to 134 aa.
- Alignment No. 13897
- 7 transmembrane receptor (rhodopsin family)
- Location within SEQ ID NO 2071: from 61 to 116 aa.
- Alignment No. 13898
- 7 transmembrane receptor (rhodopsin family)
- Location within SEQ ID NO 2071: from 61 to 140 aa.
- Alignment No. 13899
- 7 transmembrane receptor (rhodopsin family)Location within SEQ ID NO 2071: from 61 to 147 aa.
- Alignment No. 13900
- 7 transmembrane receptor (rhodopsin family)
- Location within SEQ ID NO 2071: from 61 to 150 aa.
- Alignment No. 13901
- 7 transmembrane receptor (rhodopsin family)
- Location within SEQ ID NO 2071: from 61 to 153 aa.

(D) Related Amino Acid Sequences

- Alignment No. 13902
- gi No. 100687
- % Identity 70.6
- Alignment Length 138
- Location of Alignment in SEQ ID NO 2071: from 32 to 153
- Alignment No. 13903
- gi No. 228937
- % Identity 91.5
- Alignment Length 136
- Location of Alignment in SEQ ID NO 2071: from 28 to 153
- Alignment No. 13904
- gi No. 228938
- % Identity 93.3
- Alignment Length 134
- Location of Alignment in SEQ ID NO 2071: from 28 to 153
- Alignment No. 13905
- qi No. 283032

- % Identity 96.2
- Alignment Length 130
- Location of Alignment in SEQ ID NO 2071: from 28 to 153
- Alignment No. 13906
- gi No. 283045
- % Identity 91.9
- Alignment Length 136
- Location of Alignment in SEQ ID NO 2071: from 28 to 153
- Alignment No. 13907
- gi No. 458468
- % Identity 71.8
- Alignment Length 39
- Location of Alignment in SEQ ID NO 2071: from 107 to 141
- Alignment No. 13908
- gi No. 458468
- % Identity 75.7
- Alignment Length 39
- Location of Alignment in SEQ ID NO 2071: from 118 to 153
- Alignment No. 13909
- gi No. 458468
- % Identity 76.3
- Alignment Length 40
- Location of Alignment in SEQ ID NO 2071: from 112 to 149
- Alignment No. 13910
- gi No. 458468
- % Identity 75
- Alignment Length 43
- Location of Alignment in SEQ ID NO 2071: from 112 to 151
- Alignment No. 13911
- gi No. 458468
- % Identity 72.5
- Alignment Length 43
- Location of Alignment in SEQ ID NO 2071: from 112 to 151
- Alignment No. 13912
- gi No. 458468
- % Identity 71.4
- Alignment Length 44
- Location of Alignment in SEQ ID NO 2071: from 107 to 148
- Alignment No. 13913
- gi No. 82698
- % Identity 91.6
- Alignment Length 137
- Location of Alignment in SEQ ID NO 2071: from 28 to 153
- (B) Polypeptide Sequence
 - Pat. Appln. SEQ ID NO 2072
 - Ceres seq_id 1502076
 - Location of start within SEQ ID NO 2070: at 80 nt.
- (C) Nomination and Annotation of Domains within Predicted Polypeptide(s) $% \left(\frac{1}{2}\right) =\frac{1}{2}\left(\frac{1}{2}\right) +\frac{1}{2}\left(\frac{1}{2}\right) +\frac{$
 - Alignment No. 13914
 - Collagen triple helix repeat (20 copies)

- Location within SEQ ID NO 2072: from 44 to 94 aa.
- Alignment No. 13915
- Mucin-like glycoprotein
- Location within SEQ ID NO 2072: from 8 to 127 aa.
- Alignment No. 13916
- Mucin-like glycoprotein
- Location within SEQ ID NO 2072: from 32 to 122 aa.
- Alignment No. 13917
- Mucin-like glycoprotein
- Location within SEQ ID NO 2072: from 32 to 125 aa.
- Alignment No. 13918
- 7 transmembrane receptor (rhodopsin family)
- Location within SEQ ID NO 2072: from 15 to 127 aa.
- Alignment No. 13919
- 7 transmembrane receptor (rhodopsin family)
- Location within SEQ ID NO 2072: from 22 to 127 aa.
- Alignment No. 13920
- 7 transmembrane receptor (rhodopsin family)
- Location within SEQ ID NO 2072: from 33 to 108 aa.
- Alignment No. 13921
- 7 transmembrane receptor (rhodopsin family)
- Location within SEQ ID NO 2072: from 35 to 90 aa.
- Alignment No. 13922
- 7 transmembrane receptor (rhodopsin family)
- Location within SEQ ID NO 2072: from 35 to 114 aa.
- Alignment No. 13923
- 7 transmembrane receptor (rhodopsin family)
- Location within SEQ ID NO 2072: from 35 to 121 aa.
- Alignment No. 13924
- 7 transmembrane receptor (rhodopsin family)
- Location within SEQ ID NO 2072: from 35 to 124 aa.
- Alignment No. 13925
- 7 transmembrane receptor (rhodopsin family)
- Location within SEQ ID NO 2072: from 35 to 127 aa.
- (D) Related Amino Acid Sequences
 - Alignment No. 13926
 - gi No. 100687
 - % Identity 70.6
 - Alignment Length 138
 - Location of Alignment in SEQ ID NO 2072: from 6 to 127
 - Alignment No. 13927
 - gi No. 228937
 - % Identity 91.5
 - Alignment Length 136
 - Location of Alignment in SEQ ID NO 2072: from 2 to 127
 - Alignment No. 13928
 - gi No. 228938

- % Identity 93.3 - Alignment Length 134
- Location of Alignment in SEQ ID NO 2072: from 2 to 127
- Alignment No. 13929
- gi No. 283032
- % Identity 96.2
- Alignment Length 130
- Location of Alignment in SEQ ID NO 2072: from 2 to 127
- Alignment No. 13930
- gi No. 283045
- % Identity 91.9
- Alignment Length 136
- Location of Alignment in SEQ ID NO 2072: from 2 to 127
- Alignment No. 13931
- gi No. 458468
- % Identity 71.8
- Alignment Length 39
- Location of Alignment in SEQ ID NO 2072: from 81 to 115
- Alignment No. 13932
- gi No. 458468
- % Identity 75.7
- Alignment Length 39
- Location of Alignment in SEQ ID NO 2072: from 92 to 127
- Alignment No. 13933
- gi No. 458468
- % Identity 76.3
- Alignment Length 40
- Location of Alignment in SEQ ID NO 2072: from 86 to 123
- Alignment No. 13934
- gi No. 458468
- % Identity 75
- Alignment Length 43
- Location of Alignment in SEQ ID NO 2072: from 86 to 125
- Alignment No. 13935
- gi No. 458468
- % Identity 72.5
- Alignment Length 43
- Location of Alignment in SEQ ID NO 2072: from 86 to 125
- Alignment No. 13936
- gi No. 458468
- % Identity 71.4
- Alignment Length 44
- Location of Alignment in SEQ ID NO 2072: from 81 to 122
- Alignment No. 13937
- gi No. 82698
- % Identity 91.6
- Alignment Length 137
- Location of Alignment in SEQ ID NO 2072: from 2 to 127
- (B) Polypeptide Sequence
 - Pat. Appln. SEQ ID NO 2073
 - Ceres seq_id 1502077

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- Location of start within SEQ ID NO 2070: at 83 nt.
- (C) Nomination and Annotation of Domains within Predicted Polypeptide(s)
 - Alignment No. 13938
 - Collagen triple helix repeat (20 copies)
 - Location within SEQ ID NO 2073: from 43 to 93 aa.
 - Alignment No. 13939
 - Mucin-like glycoprotein
 - Location within SEQ ID NO 2073: from 7 to 126 aa.
 - Alignment No. 13940
 - Mucin-like glycoprotein
 - Location within SEQ ID NO 2073: from 31 to 121 aa.
 - Alignment No. 13941
 - Mucin-like glycoprotein
 - Location within SEQ ID NO 2073: from 31 to 124 aa.
 - Alignment No. 13942
 - 7 transmembrane receptor (rhodopsin family)
 - Location within SEQ ID NO 2073: from 14 to 126 aa.
 - Alignment No. 13943
 - 7 transmembrane receptor (rhodopsin family)
 - Location within SEQ ID NO 2073: from 21 to 126 aa.
 - Alignment No. 13944
 - 7 transmembrane receptor (rhodopsin family)
 - Location within SEQ ID NO 2073: from 32 to 107 aa.
 - Alignment No. 13945
 - 7 transmembrane receptor (rhodopsin family)
 - Location within SEQ ID NO 2073: from 34 to 89 aa.
 - Alignment No. 13946
 - 7 transmembrane receptor (rhodopsin family)
 - Location within SEQ ID NO 2073: from 34 to 113 aa.
 - Alignment No. 13947
 - 7 transmembrane receptor (rhodopsin family)
 - Location within SEQ ID NO 2073: from 34 to 120 aa.
 - Alignment No. 13948
 - 7 transmembrane receptor (rhodopsin family)
 - Location within SEQ ID NO 2073: from 34 to 123 aa.
 - Alignment No. 13949
 - 7 transmembrane receptor (rhodopsin family)
 - Location within SEQ ID NO 2073: from 34 to 126 aa.
 - (D) Related Amino Acid Sequences
 - Alignment No. 13950
 - gi No. 100687
 - % Identity 70.6
 - Alignment Length 138
 - Location of Alignment in SEQ ID NO 2073: from 5 to 126
 - Alignment No. 13951
 - gi No. 228937

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- % Identity 91.5
- Alignment Length 136
- Location of Alignment in SEQ ID NO 2073: from 1 to 126
- Alignment No. 13952
- gi No. 228938
- % Identity 93.3
- Alignment Length 134
- Location of Alignment in SEQ ID NO 2073: from 1 to 126
- Alignment No. 13953
- gi No. 283032
- % Identity 96.2
- Alignment Length 130
- Location of Alignment in SEQ ID NO 2073: from 1 to 126
- Alignment No. 13954
- gi No. 283045
- % Identity 91.9
- Alignment Length 136
- Location of Alignment in SEQ ID NO 2073: from 1 to 126
- Alignment No. 13955
- gi No. 458468
- % Identity 71.8
- Alignment Length 39
- Location of Alignment in SEQ ID NO 2073: from 80 to 114
- Alignment No. 13956
- gi No. 458468
- % Identity 75.7
- Alignment Length 39
- Location of Alignment in SEQ ID NO 2073: from 91 to 126
- Alignment No. 13957
- gi No. 458468
- % Identity 76.3
- Alignment Length 40
- Location of Alignment in SEQ ID NO 2073: from 85 to 122
- Alignment No. 13958
- gi No. 458468
- % Identity 75
- Alignment Length 43
- Location of Alignment in SEQ ID NO 2073: from 85 to 124
- Alignment No. 13959
- gi No. 458468
- % Identity 72.5
- Alignment Length 43
- Location of Alignment in SEQ ID NO 2073: from 85 to 124
- Alignment No. 13960
- gi No. 458468
- % Identity 71.4
- Alignment Length 44
- Location of Alignment in SEQ ID NO 2073: from 80 to 121
- Alignment No. 13961
- gi No. 82698
- % Identity 91.6

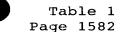
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- Alignment Length 137
- Location of Alignment in SEQ ID NO 2073: from 1 to 126

- (A) Polynucleotide Sequence
 - Pat. Appln. SEQ ID NO 2074
 - Ceres seq_id 1502086
 - (B) Polypeptide Sequence
 - Pat. Appln. SEQ ID NO 2075
 - Ceres seq_id 1502087
 - Location of start within SEQ ID NO 2074: at 222 nt.
- (C) Nomination and Annotation of Domains within Predicted Polypeptide(s) $\label{eq:condition}$
 - Alignment No. 13962
 - RNA recognition motif. (a.k.a. RRM, RBD, or RNP domain)
 - Location within SEQ ID NO 2075: from 35 to 112 aa.
 - (D) Related Amino Acid Sequences
 - Alignment No. 13963
 - gi No. 3850816
 - % Identity 77.3
 - Alignment Length 110
 - Location of Alignment in SEQ ID NO 2075: from 3 to 112
 - Alignment No. 13964
 - qi No. 3850818
 - % Identity 84.5
 - Alignment Length 110
 - Location of Alignment in SEQ ID NO 2075: from 3 to 112
 - Alignment No. 13965
 - gi No. 3850819
 - % Identity 84.5
 - Alignment Length 110
 - Location of Alignment in SEQ ID NO 2075: from 3 to 112
 - Alignment No. 13966
 - gi No. 5668775
 - % Identity 78.2
 - Alignment Length 110
 - Location of Alignment in SEQ ID NO 2075: from 3 to 112
 - (B) Polypeptide Sequence
 - Pat. Appln. SEQ ID NO 2076
 - Ceres seq_id 1502088
 - Location of start within SEQ ID NO 2074: at 294 nt.
- (C) Nomination and Annotation of Domains within Predicted Polypeptide(s) $\label{eq:continuous}$
 - Alignment No. 13967
 - RNA recognition motif. (a.k.a. RRM, RBD, or RNP domain)
 - Location within SEQ ID NO 2076: from 11 to 88 aa.
 - (D) Related Amino Acid Sequences
 - Alignment No. 13968
 - gi No. 3850816
 - % Identity 77.3
 - Alignment Length 110
 - Location of Alignment in SEQ ID NO 2076: from 1 to 88

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- Alignment No. 13969
- gi No. 3850818
- % Identity 84.5
- Alignment Length 110
- Location of Alignment in SEQ ID NO 2076: from 1 to 88
- Alignment No. 13970
- qi No. 3850819
- % Identity 84.5
- Alignment Length 110
- Location of Alignment in SEQ ID NO 2076: from 1 to 88
- Alignment No. 13971
- gi No. 5668775
- % Identity 78.2
- Alignment Length 110
- Location of Alignment in SEQ ID NO 2076: from 1 to 88
- (B) Polypeptide Sequence
 - Pat. Appln. SEQ ID NO 2077
 - Ceres seq id 1502089
 - Location of start within SEQ ID NO 2074: at 312 nt.
- (C) Nomination and Annotation of Domains within Predicted Polypeptide(s)
 - Alignment No. 13972
 - RNA recognition motif. (a.k.a. RRM, RBD, or RNP domain)
 - Location within SEQ ID NO 2077: from 5 to 82 aa.
 - (D) Related Amino Acid Sequences
 - Alignment No. 13973
 - gi No. 3850816
 - % Identity 77.3
 - Alignment Length 110
 - Location of Alignment in SEQ ID NO 2077: from 1 to 82 $\,$
 - Alignment No. 13974
 - gi No. 3850818
 - % Identity 84.5
 - Alignment Length 110
 - Location of Alignment in SEQ ID NO 2077: from 1 to 82
 - Alignment No. 13975
 - gi No. 3850819
 - % Identity 84.5
 - Alignment Length 110
 - Location of Alignment in SEQ ID NO 2077: from 1 to 82
 - Alignment No. 13976
 - gi No. 5668775
 - % Identity 78.2
 - Alignment Length 110
 - Location of Alignment in SEQ ID NO 2077: from 1 to 82

- (A) Polynucleotide Sequence
 - Pat. Appln. SEQ ID NO 2078
 - Ceres seq_id 1502090
 - (B) Polypeptide Sequence
 - Pat. Appln. SEQ ID NO 2079
 - Ceres seq_id 1502091

- Location of start within SEQ ID NO 2078: at 1 nt.
- - (D) Related Amino Acid Sequences
 - Alignment No. 13977
 - qi No. 2134207
 - % Identity 72.7
 - Alignment Length 22
 - Location of Alignment in SEQ ID NO 2079: from 71 to 92
 - Alignment No. 13978
 - gi No. 2134208
 - % Identity 72.7
 - Alignment Length 22
 - Location of Alignment in SEQ ID NO 2079: from 71 to 92
 - Alignment No. 13979
 - gi No. 2134209
 - % Identity 72.7
 - Alignment Length 22
 - Location of Alignment in SEQ ID NO 2079: from 71 to 92
 - Alignment No. 13980
 - gi No. 2134210
 - % Identity 70.8
 - Alignment Length 24
 - Location of Alignment in SEQ ID NO 2079: from 71 to 92
 - Alignment No. 13981
 - gi No. 2134211
 - % Identity 72.7
 - Alignment Length 22
 - Location of Alignment in SEQ ID NO 2079: from 71 to 92
 - (B) Polypeptide Sequence
 - Pat. Appln. SEQ ID NO 2080
 - Ceres seq_id 1502092
 - Location of start within SEQ ID NO 2078: at 3 nt.
- (C) Nomination and Annotation of Domains within Predicted Polypeptide(s)
 - (D) Related Amino Acid Sequences
 - (B) Polypeptide Sequence
 - Pat. Appln. SEQ ID NO 2081
 - Ceres seq_id 1502093
 - Location of start within SEQ ID NO 2078: at 137 nt.
- - (D) Related Amino Acid Sequences

- (A) Polynucleotide Sequence
 - Pat. Appln. SEQ ID NO 2082
 - Ceres seq_id 1502094
 - (B) Polypeptide Sequence
 - Pat. Appln. SEQ ID NO 2083
 - Ceres seq_id 1502095
 - Location of start within SEQ ID NO 2082: at 2 nt.

- (C) Nomination and Annotation of Domains within Predicted Polypeptide(s) $\label{eq:condition} % \begin{subarray}{ll} \end{subarray} % \begin{sub$
 - Alignment No. 13982
 - Glutathione S-transferases.
 - Location within SEQ ID NO 2083: from 32 to 211 aa.
 - (D) Related Amino Acid Sequences
 - (B) Polypeptide Sequence
 - Pat. Appln. SEQ ID NO 2084
 - Ceres seq id 1502096
 - Location of start within SEQ ID NO 2082: at 20 nt.
- - Alignment No. 13983
 - Glutathione S-transferases.
 - Location within SEQ ID NO 2084: from 26 to 205 aa.
 - (D) Related Amino Acid Sequences
 - (B) Polypeptide Sequence
 - Pat. Appln. SEQ ID NO 2085
 - Ceres seq_id 1502097
 - Location of start within SEQ ID NO 2082: at 50 nt.
- - Alignment No. 13984
 - Glutathione S-transferases.
 - Location within SEQ ID NO 2085: from 16 to 195 aa.
 - (D) Related Amino Acid Sequences

- (A) Polynucleotide Sequence
 - Pat. Appln. SEQ ID NO 2086
 - Ceres seq id 1502100
 - (B) Polypeptide Sequence
 - Pat. Appln. SEQ ID NO 2087
 - Ceres seq_id 1502101
 - Location of start within SEQ ID NO 2086: at 53 nt.
- - (D) Related Amino Acid Sequences
 - (B) Polypeptide Sequence
 - Pat. Appln. SEQ ID NO 2088
 - Ceres seq_id 1502102
 - Location of start within SEQ ID NO 2086: at 171 nt.
- - Alignment No. 13985
 - Pentapeptide repeats (8 copies)
 - Location within SEQ ID NO 2088: from 101 to 135 aa.
 - (D) Related Amino Acid Sequences

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- (A) Polynucleotide Sequence
 - Pat. Appln. SEQ ID NO 2089
 - Ceres seq_id 1502130
 - (B) Polypeptide Sequence
 - Pat. Appln. SEQ ID NO 2090
 - Ceres seq id 1502131
 - Location of start within SEQ ID NO 2089: at 1 nt.
- (C) Nomination and Annotation of Domains within Predicted Polypeptide(s)
 - (D) Related Amino Acid Sequences
 - Alignment No. 13986
 - gi No. 1352442
 - % Identity 79.4
 - Alignment Length 102
 - Location of Alignment in SEQ ID NO 2090: from 55 to 155
 - Alignment No. 13987
 - gi No. 170753
 - % Identity 79.4
 - Alignment Length 102
 - Location of Alignment in SEQ ID NO 2090: from 55 to 155
 - Alignment No. 13988
 - gi No. 3342823
 - % Identity 84.8
 - Alignment Length 99
 - Location of Alignment in SEQ ID NO 2090: from 58 to 155
 - Alignment No. 13989
 - gi No. 547713
 - % Identity 79.4
 - Alignment Length 102
 - Location of Alignment in SEQ ID NO 2090: from 55 to 155
 - (B) Polypeptide Sequence
 - Pat. Appln. SEQ ID NO 2091
 - Ceres seq_id 1502132
 - Location of start within SEQ ID NO 2089: at 163 nt.
- (C) Nomination and Annotation of Domains within Predicted Polypeptide(s) $% \left(\frac{1}{2}\right) =\frac{1}{2}\left(\frac{1}{2}\right) +\frac{1}{2}\left(\frac{1}{2}\right) +\frac{$
 - (D) Related Amino Acid Sequences
 - Alignment No. 13990
 - gi No. 1352442
 - % Identity 79.4
 - Alignment Length 102
 - Location of Alignment in SEQ ID NO 2091: from 1 to 101
 - Alignment No. 13991
 - gi No. 170753
 - % Identity 79.4
 - Alignment Length 102
 - Location of Alignment in SEQ ID NO 2091: from 1 to 101
 - Alignment No. 13992
 - gi No. 3342823
 - % Identity 84.8
 - Alignment Length 99
 - Location of Alignment in SEQ ID NO 2091: from 4 to 101

- Alignment No. 13993
- gi No. 547713
- % Identity 79.4
- Alignment Length 102
- Location of Alignment in SEQ ID NO 2091: from 1 to 101

- (A) Polynucleotide Sequence
 - Pat. Appln. SEQ ID NO 2092
 - Ceres seq_id 1502133
 - (B) Polypeptide Sequence
 - Pat. Appln. SEQ ID NO 2093
 - Ceres seq_id 1502134
 - Location of start within SEQ ID NO 2092: at 2 nt.
- - (D) Related Amino Acid Sequences
 - (B) Polypeptide Sequence
 - Pat. Appln. SEQ ID NO 2094
 - Ceres seq_id 1502135
 - Location of start within SEQ ID NO 2092: at 3 nt.
- (C) Nomination and Annotation of Domains within Predicted Polypeptide(s)
 - Alignment No. 13994
 - Protamine Pl
 - Location within SEQ ID NO 2094: from 22 to 94 aa.
 - (D) Related Amino Acid Sequences
 - (B) Polypeptide Sequence
 - Pat. Appln. SEQ ID NO 2095
 - Ceres seq_id 1502136
 - Location of start within SEQ ID NO 2092: at 247 nt.
- (C) Nomination and Annotation of Domains within Predicted Polypeptide(s)
 - Alignment No. 13995
 - Eukaryotic protein kinase domain
 - Location within SEQ ID NO 2095: from 23 to 88 aa.
 - (D) Related Amino Acid Sequences
 - Alignment No. 13996
 - gi No. 266410
 - % Identity 82.9
 - Alignment Length 82
 - Location of Alignment in SEQ ID NO 2095: from 7 to 88

- (A) Polynucleotide Sequence
 - Pat. Appln. SEQ ID NO 2096
 - Ceres seq_id 1502153
 - (B) Polypeptide Sequence
 - Pat. Appln. SEQ ID NO 2097
 - Ceres seq_id 1502154
 - Location of start within SEQ ID NO 2096: at 1 nt.

- - Alignment No. 13997
 - Cytochrome P450
 - Location within SEQ ID NO 2097: from 66 to 173 aa.
 - (D) Related Amino Acid Sequences
 - Alignment No. 13998
 - gi No. 1870203
 - % Identity 99.4
 - Alignment Length 165
 - Location of Alignment in SEQ ID NO 2097: from 10 to 173
 - Alignment No. 13999
 - gi No. 5420116
 - % Identity 99.4
 - Alignment Length 164
 - Location of Alignment in SEQ ID NO 2097: from 11 to 173
 - (B) Polypeptide Sequence
 - Pat. Appln. SEQ ID NO 2098
 - Ceres seq id 1502155
 - Location of start within SEQ ID NO 2096: at 28 nt.
- (C) Nomination and Annotation of Domains within Predicted Polypeptide(s)
 - Alignment No. 14000
 - Cytochrome P450
 - Location within SEQ ID NO 2098: from 57 to 164 aa.
 - (D) Related Amino Acid Sequences
 - Alignment No. 14001
 - gi No. 1870203
 - % Identity 99.4
 - Alignment Length 165
 - Location of Alignment in SEQ ID NO 2098: from 1 to 164
 - Alignment No. 14002
 - gi No. 5420116
 - % Identity 99.4
 - Alignment Length 164
 - Location of Alignment in SEQ ID NO 2098: from 2 to 164

- (A) Polynucleotide Sequence
 - Pat. Appln. SEQ ID NO 2099
 - Ceres seq_id 1502165
 - (B) Polypeptide Sequence
 - Pat. Appln. SEQ ID NO 2100
 - Ceres seq_id 1502166
 - Location of start within SEQ ID NO 2099: at 2 nt.
- - (D) Related Amino Acid Sequences
 - (B) Polypeptide Sequence
 - Pat. Appln. SEQ ID NO 2101
 - Ceres seq_id 1502167
 - Location of start within SEQ ID NO 2099: at 177 nt.

- (C) Nomination and Annotation of Domains within Predicted Polypeptide(s)
 - Alignment No. 14003
 - RNA recognition motif. (a.k.a. RRM, RBD, or RNP domain)
 - Location within SEQ ID NO 2101: from 60 to 126 aa.
 - (D) Related Amino Acid Sequences

- (A) Polynucleotide Sequence
 - Pat. Appln. SEQ ID NO 2102
 - Ceres seq_id 1502168
 - (B) Polypeptide Sequence
 - Pat. Appln. SEQ ID NO 2103
 - Ceres seq_id 1502169
 - Location of start within SEQ ID NO 2102: at 3 nt.
- - Alignment No. 14004
 - 3-beta hydroxysteroid dehydrogenase/isomerase family
 - Location within SEQ ID NO 2103: from 18 to 153 aa.
 - Alignment No. 14005
 - NAD dependent epimerase/dehydratase family
 - Location within SEQ ID NO 2103: from 21 to 140 aa.
 - (D) Related Amino Acid Sequences
 - Alignment No. 14006
 - gi No. 3269286
 - % Identity 70.6
 - Alignment Length 34
 - Location of Alignment in SEQ ID NO 2103: from 19 to 52
 - Alignment No. 14007
 - gi No. 553035
 - % Identity 74.2
 - Alignment Length 31
 - Location of Alignment in SEQ ID NO 2103: from 20 to 50
 - (B) Polypeptide Sequence
 - Pat. Appln. SEQ ID NO 2104
 - Ceres seq_id 1502170
 - Location of start within SEQ ID NO 2102: at 42 nt.
- (C) Nomination and Annotation of Domains within Predicted Polypeptide(s)
 - Alignment No. 14008
 - 3-beta hydroxysteroid dehydrogenase/isomerase family
 - Location within SEQ ID NO 2104: from 5 to 140 aa.
 - Alignment No. 14009
 - NAD dependent epimerase/dehydratase family
 - Location within SEQ ID NO 2104: from 8 to 127 aa.
 - (D) Related Amino Acid Sequences
 - Alignment No. 14010
 - gi No. 3269286
 - % Identity 70.6
 - Alignment Length 34
 - Location of Alignment in SEQ ID NO 2104: from 6 to 39

- Alignment No. 14011
- gi No. 553035
- % Identity 74.2
- Alignment Length 31
- Location of Alignment in SEQ ID NO 2104: from 7 to 37

- (A) Polynucleotide Sequence
 - Pat. Appln. SEQ ID NO 2105
 - Ceres seq id 1502189
 - (B) Polypeptide Sequence
 - Pat. Appln. SEQ ID NO 2106
 - Ceres seq_id 1502190
 - Location of start within SEQ ID NO 2105: at 192 nt.
- - Alignment No. 14012
 - Eukaryotic ribosomal protein L18
 - Location within SEQ ID NO 2106: from 14 to 165 aa.
 - (D) Related Amino Acid Sequences
 - Alignment No. 14013
 - gi No. 1172977
 - % Identity 80.9
 - Alignment Length 152
 - Location of Alignment in SEQ ID NO 2106: from 14 to 165
 - Alignment No. 14014
 - gi No. 2529670
 - % Identity 76.5
 - Alignment Length 153
 - Location of Alignment in SEQ ID NO 2106: from 14 to 165
 - Alignment No. 14015
 - gi No. 3021348
 - % Identity 80.3
 - Alignment Length 152
 - Location of Alignment in SEQ ID NO 2106: from 14 to 165
 - (B) Polypeptide Sequence
 - Pat. Appln. SEQ ID NO 2107
 - Ceres seq_id 1502191
 - Location of start within SEQ ID NO 2105: at 285 nt.
- (C) Nomination and Annotation of Domains within Predicted Polypeptide(s) $% \left(1\right) =\left(1\right) +\left(1\right) +\left$
 - Alignment No. 14016
 - Eukaryotic ribosomal protein L18
 - Location within SEQ ID NO 2107: from 1 to 134 aa.
 - (D) Related Amino Acid Sequences
 - Alignment No. 14017
 - gi No. 1172977
 - % Identity 80.9
 - Alignment Length 152
 - Location of Alignment in SEQ ID NO 2107: from 1 to 134
 - Alignment No. 14018
 - gi No. 2529670

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- % Identity 76.5
- Alignment Length 153
- Location of Alignment in SEQ ID NO 2107: from 1 to 134
- Alignment No. 14019
- gi No. 3021348
- % Identity 80.3
- Alignment Length 152
- Location of Alignment in SEQ ID NO 2107: from 1 to 134
- (B) Polypeptide Sequence
 - Pat. Appln. SEQ ID NO 2108
 - Ceres seq id 1502192
 - Location of start within SEQ ID NO 2105: at 315 nt.
- (C) Nomination and Annotation of Domains within Predicted Polypeptide(s)
 - Alignment No. 14020
 - Eukaryotic ribosomal protein L18
 - Location within SEQ ID NO 2108: from 1 to 124 aa.
 - (D) Related Amino Acid Sequences
 - Alignment No. 14021
 - gi No. 1172977
 - % Identity 80.9
 - Alignment Length 152
 - Location of Alignment in SEQ ID NO 2108: from 1 to 124
 - Alignment No. 14022
 - gi No. 2529670
 - % Identity 76.5
 - Alignment Length 153
 - Location of Alignment in SEQ ID NO 2108: from 1 to 124
 - Alignment No. 14023
 - gi No. 3021348
 - % Identity 80.3
 - Alignment Length 152
 - Location of Alignment in SEQ ID NO 2108: from 1 to 124

- (A) Polynucleotide Sequence
 - Pat. Appln. SEQ ID NO 2109
 - Ceres seq_id 1502193
 - (B) Polypeptide Sequence
 - Pat. Appln. SEQ ID NO 2110
 - Ceres seq_id 1502194
 - Location of start within SEQ ID NO 2109: at 70 nt.
- (C) Nomination and Annotation of Domains within Predicted Polypeptide(s)
 - (D) Related Amino Acid Sequences
 - Alignment No. 14024
 - gi No. 100219
 - % Identity 77.8
 - Alignment Length 18
 - Location of Alignment in SEQ ID NO 2110: from 7 to 24
 - Alignment No. 14025
 - gi No. 100219
 - % Identity 73.7

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- Alignment Length 19
- Location of Alignment in SEQ ID NO 2110: from 7 to 25
- Alignment No. 14026
- gi No. 100219
- % Identity 73.7
- Alignment Length 19
- Location of Alignment in SEQ ID NO 2110: from 7 to 25

- (A) Polynucleotide Sequence
 - Pat. Appln. SEQ ID NO 2111
 - Ceres seq_id 1502205
 - (B) Polypeptide Sequence
 - Pat. Appln. SEQ ID NO 2112
 - Ceres seq_id 1502206
 - Location of start within SEQ ID NO 2111: at 195 nt.
- (C) Nomination and Annotation of Domains within Predicted Polypeptide(s) $\label{eq:continuous}$
 - Alignment No. 14027
 - Glutathione peroxidases
 - Location within SEQ ID NO 2112: from 9 to 98 aa.
 - (D) Related Amino Acid Sequences
 - Alignment No. 14028
 - gi No. 1362150
 - % Identity 87
 - Alignment Length 46
 - Location of Alignment in SEQ ID NO 2112: from 53 to 98
 - Alignment No. 14029
 - gi No. 1708062
 - % Identity 71.7
 - Alignment Length 99
 - Location of Alignment in SEQ ID NO 2112: from 1 to 98
 - Alignment No. 14030
 - qi No. 2274857
 - % Identity 71.7
 - Alignment Length 99
 - Location of Alignment in SEQ ID NO 2112: from 1 to 98
 - Alignment No. 14031
 - gi No. 232190
 - % Identity 74.7
 - Alignment Length 99
 - Location of Alignment in SEQ ID NO 2112: from 1 to 98
 - Alignment No. 14032
 - gi No. 2388885
 - % Identity 76.8
 - Alignment Length 95
 - Location of Alignment in SEQ ID NO 2112: from 4 to 98
 - Alignment No. 14033
 - gi No. 2388887
 - % Identity 72.4
 - Alignment Length 29
 - Location of Alignment in SEQ ID NO 2112: from 70 to 98

- Alignment No. 14034
- gi No. 2392021
- % Identity 75
- Alignment Length 100
- Location of Alignment in SEQ ID NO 2112: from 1 to 98
- Alignment No. 14035
- gi No. 2632109
- % Identity 71.1
- Alignment Length 90
- Location of Alignment in SEQ ID NO 2112: from 9 to 98
- Alignment No. 14036
- gi No. 2746232
- % Identity 74
- Alignment Length 100
- Location of Alignment in SEQ ID NO 2112: from 1 to 98
- Alignment No. 14037
- qi No. 2760606
- % Identity 86.7
- Alignment Length 98
- Location of Alignment in SEQ ID NO 2112: from 1 to 98
- Alignment No. 14038
- gi No. 3023912
- % Identity 94.1
- Alignment Length 17
- Location of Alignment in SEQ ID NO 2112: from 59 to 75
- Alignment No. 14039
- gi No. 3913793
- % Identity 81.4
- Alignment Length 86
- Location of Alignment in SEQ ID NO 2112: from 13 to 98
- Alignment No. 14040
- gi No. 3913794
- % Identity 71.4
- Alignment Length 98
- Location of Alignment in SEQ ID NO 2112: from 1 to 98
- Alignment No. 14041
- gi No. 4138608
- % Identity 91.7
- Alignment Length 72
- Location of Alignment in SEQ ID NO 2112: from 1 to 72
- Alignment No. 14042
- gi No. 4584526
- % Identity 73.7
- Alignment Length 99
- Location of Alignment in SEQ ID NO 2112: from 1 to 98
- Alignment No. 14043
- gi No. 485512
- % Identity 79.2
- Alignment Length 96
- Location of Alignment in SEQ ID NO 2112: from 3 to 98
- Alignment No. 14044

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- qi No. 544437
- % Identity 80.2
- Alignment Length 96
- Location of Alignment in SEQ ID NO 2112: from 3 to 98

- (A) Polynucleotide Sequence
 - Pat. Appln. SEQ ID NO 2113
 - Ceres seq_id 1502220
 - (B) Polypeptide Sequence
 - Pat. Appln. SEQ ID NO 2114
 - Ceres seq_id 1502221
 - Location of start within SEQ ID NO 2113: at 2 nt.
- (C) Nomination and Annotation of Domains within Predicted Polypeptide(s) $\label{eq:condition}$
 - (D) Related Amino Acid Sequences
 - Alignment No. 14045
 - gi No. 1172637
 - % Identity 72.8
 - Alignment Length 81
 - Location of Alignment in SEQ ID NO 2114: from 94 to 173
 - Alignment No. 14046
 - gi No. 1172638
 - % Identity 75
 - Alignment Length 80
 - Location of Alignment in SEQ ID NO 2114: from 95 to 173
 - Alignment No. 14047
 - gi No. 1709797
 - % Identity 70.4
 - Alignment Length 81
 - Location of Alignment in SEQ ID NO 2114: from 94 to 173
 - Alignment No. 14048
 - gi No. 2492517
 - % Identity 72.8
 - Alignment Length 81
 - Location of Alignment in SEQ ID NO 2114: from 94 to 173
 - Alignment No. 14049
 - gi No. 263099
 - % Identity 72.8
 - Alignment Length 81
 - Location of Alignment in SEQ ID NO 2114: from 94 to 173
 - Alignment No. 14050
 - gi No. 2791680
 - % Identity 72.8
 - Alignment Length 81
 - Location of Alignment in SEQ ID NO 2114: from 94 to 173
 - Alignment No. 14051
 - gi No. 3450955
 - % Identity 70.4
 - Alignment Length 81
 - Location of Alignment in SEQ ID NO 2114: from 94 to 173
 - Alignment No. 14052
 - qi No. 687927

- % Identity 70
- Alignment Length 20
- Location of Alignment in SEQ ID NO 2114: from 106 to 125
- (B) Polypeptide Sequence
 - Pat. Appln. SEQ ID NO 2115
 - Ceres seq_id 1502222
 - Location of start within SEQ ID NO 2113: at 11 nt.
- - (D) Related Amino Acid Sequences
 - Alignment No. 14053
 - gi No. 1172637
 - % Identity 72.8
 - Alignment Length 81
 - Location of Alignment in SEQ ID NO 2115: from 91 to 170
 - Alignment No. 14054
 - gi No. 1172638
 - % Identity 75
 - Alignment Length 80
 - Location of Alignment in SEQ ID NO 2115: from 92 to 170
 - Alignment No. 14055
 - gi No. 1709797
 - % Identity 70.4
 - Alignment Length 81
 - Location of Alignment in SEQ ID NO 2115: from 91 to 170
 - Alignment No. 14056
 - gi No. 2492517
 - % Identity 72.8
 - Alignment Length 81
 - Location of Alignment in SEQ ID NO 2115: from 91 to 170 $\,$
 - Alignment No. 14057
 - gi No. 263099
 - % Identity 72.8
 - Alignment Length 81
 - Location of Alignment in SEQ ID NO 2115: from 91 to 170
 - Alignment No. 14058
 - gi No. 2791680
 - % Identity 72.8
 - Alignment Length 81
 - Location of Alignment in SEQ ID NO 2115: from 91 to 170
 - Alignment No. 14059
 - gi No. 3450955
 - % Identity 70.4
 - Alignment Length 81
 - Location of Alignment in SEQ ID NO 2115: from 91 to 170
 - Alignment No. 14060
 - gi No. 687927
 - % Identity 70
 - Alignment Length 20
 - Location of Alignment in SEQ ID NO 2115: from 103 to 122
 - (B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2116
- Ceres seq_id 1502223
- Location of start within SEQ ID NO 2113: at 173 nt.
- (C) Nomination and Annotation of Domains within Predicted Polypeptide(s) $% \left(\frac{1}{2}\right) =\frac{1}{2}\left(\frac{1}{2}\right) +\frac{1}{2}\left(\frac{1}{2}\right) +\frac{$
 - (D) Related Amino Acid Sequences
 - Alignment No. 14061
 - gi No. 1172637
 - % Identity 72.8
 - Alignment Length 81
 - Location of Alignment in SEQ ID NO 2116: from 37 to 116
 - Alignment No. 14062
 - gi No. 1172638
 - % Identity 75
 - Alignment Length 80
 - Location of Alignment in SEQ ID NO 2116: from 38 to 116
 - Alignment No. 14063
 - gi No. 1709797
 - % Identity 70.4
 - Alignment Length 81
 - Location of Alignment in SEQ ID NO 2116: from 37 to 116
 - Alignment No. 14064
 - gi No. 2492517
 - % Identity 72.8
 - Alignment Length 81
 - Location of Alignment in SEQ ID NO 2116: from 37 to 116
 - Alignment No. 14065
 - gi No. 263099
 - % Identity 72.8
 - Alignment Length 81
 - Location of Alignment in SEQ ID NO 2116: from 37 to 116
 - Alignment No. 14066
 - gi No. 2791680
 - % Identity 72.8
 - Alignment Length 81
 - Location of Alignment in SEQ ID NO 2116: from 37 to 116
 - Alignment No. 14067
 - gi No. 3450955
 - % Identity 70.4
 - Alignment Length 81
 - Location of Alignment in SEQ ID NO 2116: from 37 to 116
 - Alignment No. 14068
 - gi No. 687927
 - % Identity 70
 - Alignment Length 20
 - Location of Alignment in SEQ ID NO 2116: from 49 to 68

- (A) Polynucleotide Sequence
 - Pat. Appln. SEQ ID NO 2117
 - Ceres seq_id 1502224
 - (B) Polypeptide Sequence
 - Pat. Appln. SEQ ID NO 2118

- Ceres seq_id 1502225
- Location of start within SEQ ID NO 2117: at 167 nt.
- - Alignment No. 14069
 - Acetyltransferase (GNAT) family
 - Location within SEQ ID NO 2118: from 110 to 183 aa.
 - (D) Related Amino Acid Sequences
 - (B) Polypeptide Sequence
 - Pat. Appln. SEQ ID NO 2119
 - Ceres seq_id 1502226
 - Location of start within SEQ ID NO 2117: at 209 nt.
- (C) Nomination and Annotation of Domains within Predicted Polypeptide(s) $% \left(\frac{1}{2}\right) =\frac{1}{2}\left(\frac{1}{2}\right) +\frac{1}{2}\left(\frac{1}{2}\right) +\frac{$
 - Alignment No. 14070
 - Acetyltransferase (GNAT) family
 - Location within SEQ ID NO 2119: from 96 to 169 aa.
 - (D) Related Amino Acid Sequences
 - (B) Polypeptide Sequence
 - Pat. Appln. SEQ ID NO 2120
 - Ceres seq id 1502227
 - Location of start within SEQ ID NO 2117: at 272 nt.
- - Alignment No. 14071
 - Acetyltransferase (GNAT) family
 - Location within SEQ ID NO 2120: from 75 to 148 aa.
 - (D) Related Amino Acid Sequences

- (A) Polynucleotide Sequence
 - Pat. Appln. SEQ ID NO 2121
 - Ceres seq id 1502228
 - (B) Polypeptide Sequence
 - Pat. Appln. SEQ ID NO 2122
 - Ceres seq_id 1502229
 - Location of start within SEQ ID NO 2121: at 3 nt.
- - (D) Related Amino Acid Sequences
 - (B) Polypeptide Sequence
 - Pat. Appln. SEQ ID NO 2123
 - Ceres seq_id 1502230
 - Location of start within SEQ ID NO 2121: at 79 nt.
- (C) Nomination and Annotation of Domains within Predicted Polypeptide(s)
 - Alignment No. 14072
 - Pollen allergen
 - Location within SEQ ID NO 2123: from 28 to 105 aa.

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- (D) Related Amino Acid Sequences
- (B) Polypeptide Sequence
 - Pat. Appln. SEQ ID NO 2124
 - Ceres seq_id 1502231
 - Location of start within SEQ ID NO 2121: at 115 nt.
- (C) Nomination and Annotation of Domains within Predicted Polypeptide(s)
 - Alignment No. 14073
 - Pollen allergen
 - Location within SEQ ID NO 2124: from 16 to 93 aa.
 - (D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 311105 (A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 2125
- Ceres seq_id 1502270
- (B) Polypeptide Sequence
 - Pat. Appln. SEQ ID NO 2126
 - Ceres seq id 1502271
 - Location of start within SEQ ID NO 2125: at 3 nt.
- (C) Nomination and Annotation of Domains within Predicted Polypeptide(s)
 - Alignment No. 14074
 - Ras family
 - Location within SEQ ID NO 2126: from 31 to 158 aa.
 - Alignment No. 14075
 - ADP-ribosylation factor family
 - Location within SEQ ID NO 2126: from 31 to 148 aa.
 - (D) Related Amino Acid Sequences
 - Alignment No. 14076
 - gi No. 1370172
 - % Identity 72.9
 - Alignment Length 140
 - Location of Alignment in SEQ ID NO 2126: from 20 to 158
 - Alignment No. 14077
 - gi No. 2723477
 - % Identity 75.2
 - Alignment Length 141
 - Location of Alignment in SEQ ID NO 2126: from 19 to 158
 - (B) Polypeptide Sequence
 - Pat. Appln. SEQ ID NO 2127
 - Ceres seq_id 1502272
 - Location of start within SEQ ID NO 2125: at 54 nt.
- (C) Nomination and Annotation of Domains within Predicted Polypeptide(s)
 - Alignment No. 14078
 - Ras family
 - Location within SEQ ID NO 2127: from 14 to 141 aa.
 - Alignment No. 14079
 - ADP-ribosylation factor family
 - Location within SEQ ID NO 2127: from 14 to 131 aa.

- (D) Related Amino Acid Sequences
 - Alignment No. 14080
 - gi No. 1370172
 - % Identity 72.9
 - Alignment Length 140
 - Location of Alignment in SEQ ID NO 2127: from 3 to 141
 - Alignment No. 14081
 - gi No. 2723477
 - % Identity 75.2
 - Alignment Length 141
 - Location of Alignment in SEQ ID NO 2127: from 2 to 141

- (A) Polynucleotide Sequence
 - Pat. Appln. SEQ ID NO 2128
 - Ceres seq_id 1502285
 - (B) Polypeptide Sequence
 - Pat. Appln. SEQ ID NO 2129
 - Ceres seq_id 1502286
 - Location of start within SEQ ID NO 2128: at 3 nt.
- (C) Nomination and Annotation of Domains within Predicted Polypeptide(s) $% \left(\frac{1}{2}\right) =\frac{1}{2}\left(\frac{1}{2}\right) +\frac{1}{2}\left(\frac{1}{2}\right) +\frac{$
 - (D) Related Amino Acid Sequences
 - Alignment No. 14082
 - gi No. 1002380
 - % Identity 71.4
 - Alignment Length 21
 - Location of Alignment in SEQ ID NO 2129: from 94 to 112
 - (B) Polypeptide Sequence
 - Pat. Appln. SEQ ID NO 2130
 - Ceres seq_id 1502287
 - Location of start within SEQ ID NO 2128: at 54 nt.
- (C) Nomination and Annotation of Domains within Predicted Polypeptide(s) $% \left(\frac{1}{2}\right) =\frac{1}{2}\left(\frac{1}{2}\right) +\frac{1}{2}\left(\frac{1}{2}\right) +\frac{$
 - (D) Related Amino Acid Sequences
 - Alignment No. 14083
 - gi No. 1002380
 - % Identity 71.4
 - Alignment Length 21
 - Location of Alignment in SEQ ID NO 2130: from 77 to 95
 - (B) Polypeptide Sequence
 - Pat. Appln. SEQ ID NO 2131
 - Ceres seq_id 1502288
 - Location of start within SEQ ID NO 2128: at 66 nt.
- (C) Nomination and Annotation of Domains within Predicted Polypeptide(s) $% \left(\frac{1}{2}\right) =\frac{1}{2}\left(\frac{1}{2}\right) +\frac{1}{2}\left(\frac{1}{2}\right) +\frac{$
 - (D) Related Amino Acid Sequences
 - Alignment No. 14084
 - gi No. 1002380
 - % Identity 71.4
 - Alignment Length 21
 - Location of Alignment in SEQ ID NO 2131: from 73 to 91

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- (A) Polynucleotide Sequence
 - Pat. Appln. SEQ ID NO 2132
 - Ceres seq_id 1502297
 - (B) Polypeptide Sequence
 - Pat. Appln. SEQ ID NO 2133
 - Ceres seq_id 1502298
 - Location of start within SEQ ID NO 2132: at 2 nt.
- (C) Nomination and Annotation of Domains within Predicted Polypeptide(s)
 - (D) Related Amino Acid Sequences
 - (B) Polypeptide Sequence
 - Pat. Appln. SEQ ID NO 2134
 - Ceres seq id 1502299
 - Location of start within SEQ ID NO 2132: at 3 nt.
- (C) Nomination and Annotation of Domains within Predicted Polypeptide(s)
 - (D) Related Amino Acid Sequences
 - Alignment No. 14085
 - gi No. 102706
 - % Identity 75
 - Alignment Length 16
 - Location of Alignment in SEQ ID NO 2134: from 81 to 96
 - (B) Polypeptide Sequence
 - Pat. Appln. SEQ ID NO 2135
 - Ceres seq_id 1502300
 - Location of start within SEQ ID NO 2132: at 48 nt.
- (C) Nomination and Annotation of Domains within Predicted Polypeptide(s)
 - (D) Related Amino Acid Sequences
 - Alignment No. 14086
 - gi No. 102706
 - % Identity 75
 - Alignment Length 16
 - Location of Alignment in SEQ ID NO 2135: from 66 to 81

- (A) Polynucleotide Sequence
 - Pat. Appln. SEQ ID NO 2136 - Ceres seq id 1502315

 - (B) Polypeptide Sequence
 - Pat. Appln. SEQ ID NO 2137
 - Ceres seq_id 1502316
 - Location of start within SEQ ID NO 2136: at 63 nt.
- (C) Nomination and Annotation of Domains within Predicted Polypeptide(s)
 - (D) Related Amino Acid Sequences
 - Alignment No. 14087
 - gi No. 2739368
 - % Identity 71.1
 - Alignment Length 76
 - Location of Alignment in SEQ ID NO 2137: from 56 to 130
 - (B) Polypeptide Sequence
 - Pat. Appln. SEQ ID NO 2138
 - Ceres seq_id 1502317

- Location of start within SEQ ID NO 2136: at 228 nt.
- (C) Nomination and Annotation of Domains within Predicted Polypeptide(s) $% \left(\frac{1}{2}\right) =\frac{1}{2}\left(\frac{1}{2}\right) +\frac{1}{2}\left(\frac{1}{2}\right) +\frac{$
 - (D) Related Amino Acid Sequences
 - Alignment No. 14088
 - gi No. 2739368
 - % Identity 71.1
 - Alignment Length 76
 - Location of Alignment in SEQ ID NO 2138: from 1 to 75

- (A) Polynucleotide Sequence
 - Pat. Appln. SEQ ID NO 2139
 - Ceres seq_id 1502363
 - (B) Polypeptide Sequence
 - Pat. Appln. SEQ ID NO 2140
 - Ceres seq_id 1502364
 - Location of start within SEQ ID NO 2139: at 1 nt.
- (C) Nomination and Annotation of Domains within Predicted Polypeptide(s) $% \left(\frac{1}{2}\right) =\frac{1}{2}\left(\frac{1}{2}\right) +\frac{1}{2}\left(\frac{1}{2}\right) +\frac{$
 - (D) Related Amino Acid Sequences
 - Alignment No. 14089
 - gi No. 396749
 - % Identity 71.4
 - Alignment Length 21
 - Location of Alignment in SEQ ID NO 2140: from 84 to 101
 - (B) Polypeptide Sequence
 - Pat. Appln. SEQ ID NO 2141
 - Ceres seq_id 1502365
 - Location of start within SEQ ID NO 2139: at 2 nt.
- (C) Nomination and Annotation of Domains within Predicted Polypeptide(s) $\,$
 - (D) Related Amino Acid Sequences
 - (B) Polypeptide Sequence
 - Pat. Appln. SEQ ID NO 2142
 - Ceres seq_id 1502366
 - Location of start within SEQ ID NO 2139: at 3 nt.
- (C) Nomination and Annotation of Domains within Predicted Polypeptide(s) $% \left(\frac{1}{2}\right) =\frac{1}{2}\left(\frac{1}{2}\right) +\frac{1}{2}\left(\frac{1}{2}\right) +\frac{$
 - (D) Related Amino Acid Sequences
 - Alignment No. 14090
 - gi No. 2828285
 - % Identity 76.2
 - Alignment Length 21
 - Location of Alignment in SEQ ID NO 2142: from 138 to 157
 - Alignment No. 14091
 - qi No. 2832638
 - % Identity 76.2
 - Alignment Length 21
 - Location of Alignment in SEQ ID NO 2142: from 138 to 157

- (A) Polynucleotide Sequence
 - Pat. Appln. SEQ ID NO 2143

- Ceres seq_id 1502367
- (B) Polypeptide Sequence
 - Pat. Appln. SEQ ID NO 2144
 - Ceres seq_id 1502368
 - Location of start within SEQ ID NO 2143: at 3 nt.
- (C) Nomination and Annotation of Domains within Predicted Polypeptide(s) $% \left(\frac{1}{2}\right) =\frac{1}{2}\left(\frac{1}{2}\right) +\frac{1}{2}\left(\frac{1}{2}\right) +\frac{$
 - Alignment No. 14092
 - Kinesin motor domain
 - Location within SEQ ID NO 2144: from 1 to 78 aa.
 - (D) Related Amino Acid Sequences
 - Alignment No. 14093
 - gi No. 1170619
 - % Identity 89.7
 - Alignment Length 78
 - Location of Alignment in SEQ ID NO 2144: from 1 to 78
 - Alignment No. 14094
 - gi No. 1170620
 - % Identity 88.5
 - Alignment Length 78
 - Location of Alignment in SEQ ID NO 2144: from 1 to 78
 - Alignment No. 14095
 - gi No. 1170621
 - % Identity 87.2
 - Alignment Length 78
 - Location of Alignment in SEQ ID NO 2144: from 1 to 78
 - Alignment No. 14096
 - gi No. 125477
 - % Identity 70.9
 - Alignment Length 79
 - Location of Alignment in SEQ ID NO 2144: from 1 to 77
 - Alignment No. 14097
 - gi No. 2826849
 - % Identity 73.3
 - Alignment Length 15
 - Location of Alignment in SEQ ID NO 2144: from 1 to 15
 - Alignment No. 14098
 - gi No. 3023586
 - % Identity 70.1
 - Alignment Length 77
 - Location of Alignment in SEQ ID NO 2144: from 1 to 77
 - Alignment No. 14099
 - gi No. 3913957
 - % Identity 73.3
 - Alignment Length 15
 - Location of Alignment in SEQ ID NO 2144: from 1 to 15
 - Alignment No. 14100
 - gi No. 4490714
 - % Identity 88.5
 - Alignment Length 78
 - Location of Alignment in SEQ ID NO 2144: from 1 to 78

- Alignment No. 14101
- gi No. 4504869
- % Identity 73.3
- Alignment Length 15
- Location of Alignment in SEQ ID NO 2144: from 1 to 15

Maximum Length Sequence corresponding to clone ID 311460 (A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 2145
 - Ceres seq_id 1502373
 - (B) Polypeptide Sequence
 - Pat. Appln. SEQ ID NO 2146
 - Ceres seq_id 1502374
 - Location of start within SEQ ID NO 2145: at 2 nt.
- (C) Nomination and Annotation of Domains within Predicted Polypeptide(s)
 - (D) Related Amino Acid Sequences
 - (B) Polypeptide Sequence
 - Pat. Appln. SEQ ID NO 2147
 - Ceres seq_id 1502375
 - Location of start within SEQ ID NO 2145: at 188 nt.
- - (D) Related Amino Acid Sequences
 - Alignment No. 14102
 - gi No. 2655291
 - % Identity 82.1
 - Alignment Length 67
 - Location of Alignment in SEQ ID NO 2147: from 1 to 66
 - Alignment No. 14103
 - gi No. 2979494
 - % Identity 73
 - Alignment Length 37
 - Location of Alignment in SEQ ID NO 2147: from 22 to 58
 - (B) Polypeptide Sequence
 - Pat. Appln. SEQ ID NO 2148
 - Ceres seq_id 1502376
 - Location of start within SEQ ID NO 2145: at 272 nt.
- (C) Nomination and Annotation of Domains within Predicted Polypeptide(s) $\label{eq:condition}$
 - (D) Related Amino Acid Sequences
 - Alignment No. 14104
 - gi No. 2655291
 - % Identity 82.1
 - Alignment Length 67
 - Location of Alignment in SEQ ID NO 2148: from 1 to 38
 - Alignment No. 14105
 - gi No. 2979494
 - % Identity 73
 - Alignment Length 37
 - Location of Alignment in SEQ ID NO 2148: from 1 to 30

Maximum Length Sequence corresponding to clone ID 311474 (A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 2149
- Ceres seq_id 1502381
- (B) Polypeptide Sequence
 - Pat. Appln. SEQ ID NO 2150
 - Ceres seq id 1502382
 - Location of start within SEQ ID NO 2149: at 1 nt.
- (C) Nomination and Annotation of Domains within Predicted Polypeptide(s)
 - Alignment No. 14106
 - Eukaryotic protein kinase domain
 - Location within SEQ ID NO 2150: from 1 to 131 aa.
 - (D) Related Amino Acid Sequences
 - Alignment No. 14107
 - gi No. 1066501
 - % Identity 70.2
 - Alignment Length 132
 - Location of Alignment in SEQ ID NO 2150: from 3 to 131
 - Alignment No. 14108
 - gi No. 1168470
 - % Identity 73.9
 - Alignment Length 135
 - Location of Alignment in SEQ ID NO 2150: from 1 to 131
 - Alignment No. 14109
 - gi No. 1168471
 - % Identity 77.4
 - Alignment Length 94
 - Location of Alignment in SEQ ID NO 2150: from 42 to 131
 - Alignment No. 14110
 - gi No. 1778444
 - % Identity 75.6
 - Alignment Length 45
 - Location of Alignment in SEQ ID NO 2150: from 88 to 131
 - Alignment No. 14111
 - gi No. 2852447
 - % Identity 72
 - Alignment Length 133
 - Location of Alignment in SEQ ID NO 2150: from 1 to 131
 - Alignment No. 14112
 - gi No. 2852449
 - % Identity 71.2
 - Alignment Length 133
 - Location of Alignment in SEQ ID NO 2150: from 1 to 131
 - Alignment No. 14113
 - gi No. 3075390
 - % Identity 76.2
 - Alignment Length 131
 - Location of Alignment in SEQ ID NO 2150: from 3 to 131
 - Alignment No. 14114
 - gi No. 3461835
 - % Identity 73.1
 - Alignment Length 135
 - Location of Alignment in SEQ ID NO 2150: from 1 to 131

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- Alignment No. 14115
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- gi No. 3805765
- % Identity 70.8
- Alignment Length 131
- Location of Alignment in SEQ ID NO 2150: from 3 to 131
- Alignment No. 14116
- gi No. 4006829
- % Identity 74.6
- Alignment Length 131
- Location of Alignment in SEQ ID NO 2150: from 3 to 131
- Alignment No. 14117
- gi No. 4432889
- % Identity 77.4
- Alignment Length 94
- Location of Alignment in SEQ ID NO 2150: from 42 to 131
- Alignment No. 14118
- gi No. 4585873
- % Identity 73.1
- Alignment Length 131
- Location of Alignment in SEQ ID NO 2150: from 3 to 131
- Alignment No. 14119
- gi No. 4753653
- % Identity 71
- Alignment Length 62
- Location of Alignment in SEQ ID NO 2150: from 69 to 130
- Alignment No. 14120
- gi No. 5091529
- % Identity 83.3
- Alignment Length 132
- Location of Alignment in SEQ ID NO 2150: from 1 to 131

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2151
- Ceres seq_id 1502383
- Location of start within SEQ ID NO 2149: at 160 nt.
- (C) Nomination and Annotation of Domains within Predicted Polypeptide(s) $% \left(\frac{1}{2}\right) =\frac{1}{2}\left(\frac{1}{2}\right) +\frac{1}{2}\left(\frac{1}{2}\right) +\frac{$
 - Alignment No. 14121
 - Eukaryotic protein kinase domain
 - Location within SEQ ID NO 2151: from 1 to 78 aa.

(D) Related Amino Acid Sequences

- Alignment No. 14122
- gi No. 1066501
- % Identity 70.2
- Alignment Length 132
- Location of Alignment in SEQ ID NO 2151: from 1 to 78
- Alignment No. 14123
- gi No. 1168470
- % Identity 73.9
- Alignment Length 135
- Location of Alignment in SEQ ID NO 2151: from 1 to 78

- Alignment No. 14124 - gi No. 1168471 - % Identity 77.4 - Alignment Length 94
- Location of Alignment in SEQ ID NO 2151: from 1 to 78
- Alignment No. 14125
- gi No. 1778444
- % Identity 75.6
- Alignment Length 45
- Location of Alignment in SEQ ID NO 2151: from 35 to 78
- Alignment No. 14126
- gi No. 2852447
- % Identity 72
- Alignment Length 133
- Location of Alignment in SEQ ID NO 2151: from 1 to 78
- Alignment No. 14127
- gi No. 2852449
- % Identity 71.2
- Alignment Length 133
- Location of Alignment in SEQ ID NO 2151: from 1 to 78
- Alignment No. 14128
- gi No. 3075390
- % Identity 76.2
- Alignment Length 131
- Location of Alignment in SEQ ID NO 2151: from 1 to 78
- Alignment No. 14129
- gi No. 3461835
- % Identity 73.1
- Alignment Length 135
- Location of Alignment in SEQ ID NO 2151: from 1 to 78
- Alignment No. 14130
- gi No. 3805765
- % Identity 70.8
- Alignment Length 131
- Location of Alignment in SEQ ID NO 2151: from 1 to 78
- Alignment No. 14131
- qi No. 4006829
- % Identity 74.6
- Alignment Length 131
- Location of Alignment in SEQ ID NO 2151: from 1 to 78
- Alignment No. 14132
- gi No. 4432889
- % Identity 77.4
- Alignment Length 94
- Location of Alignment in SEQ ID NO 2151: from 1 to 78
- Alignment No. 14133
- gi No. 4585873
- % Identity 73.1
- Alignment Length 131
- Location of Alignment in SEQ ID NO 2151: from 1 to 78
- Alignment No. 14134

- gi No. 4753653
- % Identity 71
- Alignment Length 62
- Location of Alignment in SEQ ID NO 2151: from 16 to 77
- Alignment No. 14135
- qi No. 5091529
- % Identity 83.3
- Alignment Length 132
- Location of Alignment in SEQ ID NO 2151: from 1 to 78

- (A) Polynucleotide Sequence
 - Pat. Appln. SEQ ID NO 2152
 - Ceres seq_id 1502387
 - (B) Polypeptide Sequence
 - Pat. Appln. SEQ ID NO 2153
 - Ceres seq_id 1502388
 - Location of start within SEQ ID NO 2152: at 2 nt.
- (C) Nomination and Annotation of Domains within Predicted Polypeptide(s)
 - Alignment No. 14136
 - Ribosomal protein L5
 - Location within SEQ ID NO 2153: from 65 to 100 aa.
 - Alignment No. 14137
 - ribosomal L5P family C-terminus
 - Location within SEQ ID NO 2153: from 104 to 158 aa.
 - (D) Related Amino Acid Sequences
 - Alignment No. 14138
 - gi No. 1125808
 - % Identity 84.2
 - Alignment Length 95
 - Location of Alignment in SEQ ID NO 2153: from 65 to 158
 - Alignment No. 14139
 - gi No. 1172816
 - % Identity 96.8
 - Alignment Length 95
 - Location of Alignment in SEQ ID NO 2153: from 65 to 158
 - Alignment No. 14140
 - gi No. 1172817
 - % Identity 97.9
 - Alignment Length 95
 - Location of Alignment in SEQ ID NO 2153: from 65 to 158
 - Alignment No. 14141
 - gi No. 1172952
 - % Identity 84.2
 - Alignment Length 95
 - Location of Alignment in SEQ ID NO 2153: from 65 to 158
 - Alignment No. 14142
 - gi No. 1172954
 - % Identity 78.9
 - Alignment Length 95
 - Location of Alignment in SEQ ID NO 2153: from 65 to 158

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- Alignment No. 14143
- gi No. 1172969
- % Identity 97.9
- Alignment Length 95
- Location of Alignment in SEQ ID NO 2153: from 65 to 158
- Alignment No. 14144
- gi No. 1173055
- % Identity 100
- Alignment Length 95
- Location of Alignment in SEQ ID NO 2153: from 65 to 158
- Alignment No. 14145
- gi No. 1246369
- % Identity 74.5
- Alignment Length 94
- Location of Alignment in SEQ ID NO 2153: from 65 to 158
- Alignment No. 14146
- gi No. 132649
- % Identity 85.3
- Alignment Length 95
- Location of Alignment in SEQ ID NO 2153: from 65 to 158
- Alignment No. 14147
- gi No. 132777
- % Identity 74.7
- Alignment Length 95
- Location of Alignment in SEQ ID NO 2153: from 65 to 158
- Alignment No. 14148
- gi No. 132951
- % Identity 83.2
- Alignment Length 95
- Location of Alignment in SEQ ID NO 2153: from 65 to 158
- Alignment No. 14149
- gi No. 132992
- % Identity 77.8
- Alignment Length 63
- Location of Alignment in SEQ ID NO 2153: from 65 to 127
- Alignment No. 14150
- gi No. 1350658
- % Identity 83.2
- Alignment Length 95
- Location of Alignment in SEQ ID NO 2153: from 65 to 158
- Alignment No. 14151
- gi No. 1350659
- % Identity 77.9
- Alignment Length 95
- Location of Alignment in SEQ ID NO 2153: from 65 to 158
- Alignment No. 14152
- gi No. 1710480
- % Identity 75.8
- Alignment Length 95
- Location of Alignment in SEQ ID NO 2153: from 65 to 158
- Alignment No. 14153

- gi No. 1710494 - % Identity 87.4 - Alignment Length 95 - Location of Alignment in SEQ ID NO 2153: from 65 to 158 - Alignment No. 14154 - gi No. 2500240 - % Identity 84 - Alignment Length 94 - Location of Alignment in SEQ ID NO 2153: from 65 to 158 - Alignment No. 14155 - gi No. 2500241 - % Identity 81.3 - Alignment Length 91 - Location of Alignment in SEQ ID NO 2153: from 65 to 155 - Alignment No. 14156 - gi No. 2570507 - % Identity 89.5 - Alignment Length 95 - Location of Alignment in SEQ ID NO 2153: from 65 to 158 - Alignment No. 14157 - gi No. 3914659 - % Identity 84.2 - Alignment Length 95 - Location of Alignment in SEQ ID NO 2153: from 65 to 158 - Alignment No. 14158 - qi No. 4322 - % Identity 82.1 - Alignment Length 95 - Location of Alignment in SEQ ID NO 2153: from 65 to 158 - Alignment No. 14159 - gi No. 4432750 - % Identity 96 - Alignment Length 25 - Location of Alignment in SEQ ID NO 2153: from 65 to 89 - Alignment No. 14160 - gi No. 4506595 - % Identity 81.1
- Alignment Length 95
- Location of Alignment in SEQ ID NO 2153: from 65 to 158
- Alignment No. 14161
- gi No. 4512679
- % Identity 88.6
- Alignment Length 105
- Location of Alignment in SEQ ID NO 2153: from 65 to 158
- Alignment No. 14162
- gi No. 4586222
- % Identity 85.3
- Alignment Length 95
- Location of Alignment in SEQ ID NO 2153: from 65 to 158
- Alignment No. 14163
- gi No. 71107

- % Identity 83.2
- Alignment Length 95
- Location of Alignment in SEQ ID NO 2153: from 65 to 158
- (B) Polypeptide Sequence
 - Pat. Appln. SEQ ID NO 2154
 - Ceres seq id 1502389
 - Location of start within SEQ ID NO 2152: at 117 nt.
- (C) Nomination and Annotation of Domains within Predicted Polypeptide(s)
 - (D) Related Amino Acid Sequences
 - Alignment No. 14164
 - gi No. 1172816
 - % Identity 85.7
 - Alignment Length 28
 - Location of Alignment in SEQ ID NO 2154: from 1 to 28
 - Alignment No. 14165
 - gi No. 1172817
 - % Identity 85.2
 - Alignment Length 27
 - Location of Alignment in SEQ ID NO 2154: from 2 to 28
 - Alignment No. 14166
 - gi No. 1172969
 - % Identity 85.7
 - Alignment Length 28
 - Location of Alignment in SEQ ID NO 2154: from 1 to 28
 - Alignment No. 14167
 - gi No. 1173055
 - % Identity 89.3
 - Alignment Length 28
 - Location of Alignment in SEQ ID NO 2154: from 1 to 28
 - Alignment No. 14168
 - qi No. 2570507
 - % Identity 89.3
 - Alignment Length 28
 - Location of Alignment in SEQ ID NO 2154: from 1 to 28
 - (B) Polypeptide Sequence
 - Pat. Appln. SEQ ID NO 2155
 - Ceres seq_id 1502390
 - Location of start within SEQ ID NO 2152: at 147 nt.
- - (D) Related Amino Acid Sequences
 - Alignment No. 14169
 - gi No. 1172816
 - % Identity 85.7
 - Alignment Length 28
 - Location of Alignment in SEQ ID NO 2155: from 1 to 18
 - Alignment No. 14170
 - gi No. 1172817
 - % Identity 85.2
 - Alignment Length 27
 - Location of Alignment in SEQ ID NO 2155: from 1 to 18

- Alignment No. 14171
- gi No. 1172969
- % Identity 85.7
- Alignment Length 28
- Location of Alignment in SEQ ID NO 2155: from 1 to 18
- Alignment No. 14172
- gi No. 1173055
- % Identity 89.3
- Alignment Length 28
- Location of Alignment in SEQ ID NO 2155: from 1 to 18
- Alignment No. 14173
- gi No. 2570507
- % Identity 89.3
- Alignment Length 28
- Location of Alignment in SEQ ID NO 2155: from 1 to 18

Maximum Length Sequence corresponding to clone ID 311538

- (A) Polynucleotide Sequence
 - Pat. Appln. SEQ ID NO 2156
 - Ceres seq_id 1502407
 - (B) Polypeptide Sequence
 - Pat. Appln. SEQ ID NO 2157
 - Ceres seq_id 1502408
 - Location of start within SEQ ID NO 2156: at 72 nt.
- - Alignment No. 14174
 - Peroxidase
 - Location within SEQ ID NO 2157: from 61 to 134 aa.
 - (D) Related Amino Acid Sequences
 - (B) Polypeptide Sequence
 - Pat. Appln. SEQ ID NO 2158
 - Ceres seg id 1502409
 - Location of start within SEQ ID NO 2156: at 210 nt.
- - Alignment No. 14175
 - Peroxidase
 - Location within SEQ ID NO 2158: from 15 to 88 aa.
 - (D) Related Amino Acid Sequences

- (A) Polynucleotide Sequence
 - Pat. Appln. SEQ ID NO 2159
 - Ceres seq_id 1502420
 - (B) Polypeptide Sequence
 - Pat. Appln. SEQ ID NO 2160
 - Ceres seq_id 1502421
 - Location of start within SEQ ID NO 2159: at 3 nt.
- - Alignment No. 14176



- Ribosomal protein S12
- Location within SEQ ID NO 2160: from 58 to 144 aa.

(D) Related Amino Acid Sequences

- Alignment No. 14177
- gi No. 1173187
- % Identity 97.7
- Alignment Length 88
- Location of Alignment in SEQ ID NO 2160: from 58 to 144
- Alignment No. 14178
- gi No. 1350965
- % Identity 97.7
- Alignment Length 86
- Location of Alignment in SEQ ID NO 2160: from 58 to 143
- Alignment No. 14179
- gi No. 1850766
- % Identity 74.2
- Alignment Length 89
- Location of Alignment in SEQ ID NO 2160: from 58 to 144
- Alignment No. 14180
- gi No. 2500455
- % Identity 74.2
- Alignment Length 89
- Location of Alignment in SEQ ID NO 2160: from 58 to 144
- Alignment No. 14181
- gi No. 2829742
- % Identity 81.8
- Alignment Length 88
- Location of Alignment in SEQ ID NO 2160: from 59 to 144
- Alignment No. 14182
- gi No. 2833303
- % Identity 79.5
- Alignment Length 88
- Location of Alignment in SEQ ID NO 2160: from 59 to 144
- Alignment No. 14183
- gi No. 3088342
- % Identity 92.9
- Alignment Length 28
- Location of Alignment in SEQ ID NO 2160: from 118 to 144
- Alignment No. 14184
- gi No. 417716
- % Identity 75.3
- Alignment Length 89
- Location of Alignment in SEQ ID NO 2160: from 58 to 144
- Alignment No. 14185
- gi No. 4493905
- % Identity 75.3
- Alignment Length 93
- Location of Alignment in SEQ ID NO 2160: from 54 to 144
- Alignment No. 14186
- gi No. 4506701
- % Identity 81.8

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- Alignment Length 88
- Location of Alignment in SEQ ID NO 2160: from 59 to 144

Maximum Length Sequence corresponding to clone ID 311571

- (A) Polynucleotide Sequence
 - Pat. Appln. SEQ ID NO 2161
 - Ceres seq_id 1502422
 - (B) Polypeptide Sequence
 - Pat. Appln. SEQ ID NO 2162
 - Ceres seq id 1502423
 - Location of start within SEQ ID NO 2161: at 1 nt.
- - Alignment No. 14187
 - AhpC/TSA family
 - Location within SEQ ID NO 2162: from 11 to 67 aa.
 - (D) Related Amino Acid Sequences
 - Alignment No. 14188
 - gi No. 5441879
 - % Identity 80
 - Alignment Length 40
 - Location of Alignment in SEQ ID NO 2162: from 28 to 67
 - (B) Polypeptide Sequence
 - Pat. Appln. SEQ ID NO 2163
 - Ceres seq_id 1502424
 - Location of start within SEQ ID NO 2161: at 3 nt.
- (C) Nomination and Annotation of Domains within Predicted Polypeptide(s) $\label{eq:continuous}$
 - Alignment No. 14189
 - AhpC/TSA family
 - Location within SEQ ID NO 2163: from 66 to 142 aa.
 - (D) Related Amino Acid Sequences
 - Alignment No. 14190
 - gi No. 5441879
 - % Identity 72.2
 - Alignment Length 97
 - Location of Alignment in SEQ ID NO 2163: from 65 to 159
 - (B) Polypeptide Sequence
 - Pat. Appln. SEQ ID NO 2164
 - Ceres seg id 1502425
 - Location of start within SEQ ID NO 2161: at 68 nt.
- (C) Nomination and Annotation of Domains within Predicted Polypeptide(s)
 - (D) Related Amino Acid Sequences

- (A) Polynucleotide Sequence
 - Pat. Appln. SEQ ID NO 2165
 - Ceres seq_id 1502429
 - (B) Polypeptide Sequence
 - Pat. Appln. SEQ ID NO 2166
 - Ceres seq id 1502430
 - Location of start within SEQ ID NO 2165: at 167 nt.

- (C) Nomination and Annotation of Domains within Predicted Polypeptide(s)
 - (D) Related Amino Acid Sequences
 - Alignment No. 14191
 - gi No. 417298
 - % Identity 74.7
 - Alignment Length 75
 - Location of Alignment in SEQ ID NO 2166: from 1 to 75
 - (B) Polypeptide Sequence
 - Pat. Appln. SEQ ID NO 2167
 - Ceres seq id 1502431
 - Location of start within SEQ ID NO 2165: at 185 nt.
- (C) Nomination and Annotation of Domains within Predicted Polypeptide(s)
 - (D) Related Amino Acid Sequences
 - Alignment No. 14192
 - gi No. 417298
 - % Identity 74.7
 - Alignment Length 75
 - Location of Alignment in SEQ ID NO 2167: from 1 to 69
 - (B) Polypeptide Sequence
 - Pat. Appln. SEQ ID NO 2168
 - Ceres seq_id 1502432
 - Location of start within SEQ ID NO 2165: at 188 nt.
- - (D) Related Amino Acid Sequences
 - Alignment No. 14193
 - gi No. 417298
 - % Identity 74.7
 - Alignment Length 75
 - Location of Alignment in SEQ ID NO 2168: from 1 to 68

- (A) Polynucleotide Sequence
 - Pat. Appln. SEQ ID NO 2169
 - Ceres seq_id 1502441
 - (B) Polypeptide Sequence
 - Pat. Appln. SEQ ID NO 2170
 - Ceres seq_id 1502442
 - Location of start within SEQ ID NO 2169: at 2 nt.
- (C) Nomination and Annotation of Domains within Predicted Polypeptide(s)
 - (D) Related Amino Acid Sequences
 - Alignment No. 14194
 - gi No. 3335351
 - % Identity 72.7
 - Alignment Length 11
 - Location of Alignment in SEQ ID NO 2170: from 41 to 51
 - (B) Polypeptide Sequence
 - Pat. Appln. SEQ ID NO 2171
 - Ceres seq_id 1502443
 - Location of start within SEQ ID NO 2169: at 3 nt.

- (C) Nomination and Annotation of Domains within Predicted Polypeptide(s)
 - (D) Related Amino Acid Sequences
 - Alignment No. 14195
 - gi No. 2924785
 - % Identity 72.2
 - Alignment Length 18
 - Location of Alignment in SEQ ID NO 2171: from 12 to 29

- (A) Polynucleotide Sequence
 - Pat. Appln. SEQ ID NO 2172
 - Ceres seq_id 1502461
 - (B) Polypeptide Sequence
 - Pat. Appln. SEQ ID NO 2173
 - Ceres seq_id 1502462
 - Location of start within SEQ ID NO 2172: at 1 nt.
- (C) Nomination and Annotation of Domains within Predicted Polypeptide(s)
 - (D) Related Amino Acid Sequences
 - Alignment No. 14196
 - gi No. 4028260
 - % Identity 72.7
 - Alignment Length 11
 - Location of Alignment in SEQ ID NO 2173: from 38 to 48

- (A) Polynucleotide Sequence
 - Pat. Appln. SEQ ID NO 2174
 - Ceres seq_id 1502479
 - (B) Polypeptide Sequence
 - Pat. Appln. SEQ ID NO 2175
 - Ceres seq_id 1502480
 - Location of start within SEQ ID NO 2174: at 1 nt.
- (C) Nomination and Annotation of Domains within Predicted Polypeptide(s)
 - (D) Related Amino Acid Sequences
 - (B) Polypeptide Sequence
 - Pat. Appln. SEQ ID NO 2176
 - Ceres seq_id 1502481
 - Location of start within SEQ ID NO 2174: at 3 nt.
- (C) Nomination and Annotation of Domains within Predicted Polypeptide(s)
 - Alignment No. 14197

 - Elongation factor 1 gamma, conserved domain.Location within SEQ ID NO 2176: from 29 to 81 aa.
 - (D) Related Amino Acid Sequences
 - Alignment No. 14198
 - gi No. 2160158
 - % Identity 75.9
 - Alignment Length 79
 - Location of Alignment in SEQ ID NO 2176: from 1 to 73
 - Alignment No. 14199
 - gi No. 3868758
 - % Identity 87.8

- Alignment Length 74
- Location of Alignment in SEQ ID NO 2176: from 1 to 73 $\,$
- (B) Polypeptide Sequence
 - Pat. Appln. SEQ ID NO 2177
 - Ceres seq_id 1502482
 - Location of start within SEQ ID NO 2174: at 7 nt.
- - (D) Related Amino Acid Sequences

- (A) Polynucleotide Sequence
 - Pat. Appln. SEQ ID NO 2178
 - Ceres seq_id 1502487
 - (B) Polypeptide Sequence
 - Pat. Appln. SEQ ID NO 2179
 - Ceres seq id 1502488
 - Location of start within SEQ ID NO 2178: at 102 nt.
- - Alignment No. 14200
 - G-protein alpha subunit
 - Location within SEQ ID NO 2179: from 46 to 112 aa.
 - Alignment No. 14201
 - ADP-ribosylation factor family
 - Location within SEQ ID NO 2179: from 1 to 117 aa.
 - Alignment No. 14202
 - Ras family
 - Location within SEQ ID NO 2179: from 18 to 92 aa.
 - (D) Related Amino Acid Sequences
 - Alignment No. 14203
 - gi No. 4309728
 - % Identity 91.5
 - Alignment Length 118
 - Location of Alignment in SEQ ID NO 2179: from 1 to 117
 - (B) Polypeptide Sequence
 - Pat. Appln. SEQ ID NO 2180
 - Ceres seq id 1502489
 - Location of start within SEQ ID NO 2178: at 150 nt.
- (C) Nomination and Annotation of Domains within Predicted Polypeptide(s)
 - Alignment No. 14204
 - G-protein alpha subunit
 - Location within SEQ ID NO 2180: from 30 to 96 aa.
 - Alignment No. 14205
 - ADP-ribosylation factor family
 - Location within SEQ ID NO 2180: from 1 to 101 aa.
 - Alignment No. 14206
 - Ras family
 - Location within SEQ ID NO 2180: from 2 to 76 aa.

- (D) Related Amino Acid Sequences
 - Alignment No. 14207
 - gi No. 4309728
 - % Identity 91.5
 - Alignment Length 118
 - Location of Alignment in SEQ ID NO 2180: from 1 to 101
- (B) Polypeptide Sequence
 - Pat. Appln. SEQ ID NO 2181
 - Ceres seq_id 1502490
 - Location of start within SEQ ID NO 2178: at 162 nt.
- - Alignment No. 14208
 - G-protein alpha subunit
 - Location within SEQ ID NO 2181: from 26 to 92 aa.
 - Alignment No. 14209
 - ADP-ribosylation factor family
 - Location within SEQ ID NO 2181: from 1 to 97 aa.
 - Alignment No. 14210
 - Ras family
 - Location within SEQ ID NO 2181: from 1 to 72 aa.
 - (D) Related Amino Acid Sequences
 - Alignment No. 14211
 - gi No. 4309728
 - % Identity 91.5
 - Alignment Length 118
 - Location of Alignment in SEQ ID NO 2181: from 1 to 97

- (A) Polynucleotide Sequence
 - Pat. Appln. SEQ ID NO 2182
 - Ceres seq_id 1502514
 - (B) Polypeptide Sequence
 - Pat. Appln. SEQ ID NO 2183
 - Ceres seq_id 1502515
 - Location of start within SEQ ID NO 2182: at 3 nt.
- - (D) Related Amino Acid Sequences
 - (B) Polypeptide Sequence
 - Pat. Appln. SEQ ID NO 2184
 - Ceres seq_id 1502516
 - Location of start within SEQ ID NO 2182: at 89 nt.
- (C) Nomination and Annotation of Domains within Predicted Polypeptide(s)
 - Alignment No. 14212
 - Ribosomal L29 protein
 - Location within SEQ ID NO 2184: from 6 to 69 aa.
 - (D) Related Amino Acid Sequences
 - Alignment No. 14213
 - gi No. 3355468
 - % Identity 85.2

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- Alignment Length 122
- Location of Alignment in SEQ ID NO 2184: from 1 to 122

Maximum Length Sequence corresponding to clone ID 311870

- (A) Polynucleotide Sequence
 - Pat. Appln. SEQ ID NO 2185
 - Ceres seq_id 1502517
 - (B) Polypeptide Sequence
 - Pat. Appln. SEQ ID NO 2186
 - Ceres seq_id 1502518
 - Location of start within SEQ ID NO 2185: at 3 nt.
- (C) Nomination and Annotation of Domains within Predicted Polypeptide(s) $% \left(\frac{1}{2}\right) =\frac{1}{2}\left(\frac{1}{2}\right) +\frac{1}{2}\left(\frac{1}{2}\right) +\frac{$
 - Alignment No. 14214
 - Protein-tyrosine phosphatase
 - Location within SEQ ID NO 2186: from 1 to 60 aa.
 - (D) Related Amino Acid Sequences
 - Alignment No. 14215
 - gi No. 3413473
 - % Identity 71.7
 - Alignment Length 60
 - Location of Alignment in SEQ ID NO 2186: from 1 to 60
 - Alignment No. 14216
 - gi No. 3413500
 - % Identity 73.3
 - Alignment Length 60
 - Location of Alignment in SEQ ID NO 2186: from 1 to 60
 - Alignment No. 14217
 - gi No. 348540
 - % Identity 78.6
 - Alignment Length 14
 - Location of Alignment in SEQ ID NO 2186: from 1 to 14
 - Alignment No. 14218
 - gi No. 464498
 - % Identity 78.6
 - Alignment Length 14
 - Location of Alignment in SEQ ID NO 2186: from 1 to 14

- (A) Polynucleotide Sequence
 - Pat. Appln. SEQ ID NO 2187
 - Ceres seq id 1502519
 - (B) Polypeptide Sequence
 - Pat. Appln. SEQ ID NO 2188
 - Ceres seq id 1502520
 - Location of start within SEQ ID NO 2187: at 147 nt.
- - (D) Related Amino Acid Sequences
 - (B) Polypeptide Sequence
 - Pat. Appln. SEQ ID NO 2189
 - Ceres seq_id 1502521
 - Location of start within SEQ ID NO 2187: at 197 nt.

- (C) Nomination and Annotation of Domains within Predicted Polypeptide(s)
 - (D) Related Amino Acid Sequences
 - Alignment No. 14219
 - qi No. 1769895
 - % Identity 72.4
 - Alignment Length 76
 - Location of Alignment in SEQ ID NO 2189: from 1 to 76
 - (B) Polypeptide Sequence
 - Pat. Appln. SEQ ID NO 2190
 - Ceres seq id 1502522
 - Location of start within SEQ ID NO 2187: at 218 nt.
- - (D) Related Amino Acid Sequences
 - Alignment No. 14220
 - qi No. 1769895
 - % Identity 72.4
 - Alignment Length 76
 - Location of Alignment in SEQ ID NO 2190: from 1 to 69

- (A) Polynucleotide Sequence
 - Pat. Appln. SEQ ID NO 2191
 - Ceres seq_id 1502527
 - (B) Polypeptide Sequence
 - Pat. Appln. SEQ ID NO 2192
 - Ceres seq_id 1502528
 - Location of start within SEQ ID NO 2191: at 1 nt.
- - Alignment No. 14221
 - ATPases associated with various cellular activities (AAA)
 - Location within SEQ ID NO 2192: from 1 to 62 aa.
 - (D) Related Amino Acid Sequences
 - Alignment No. 14222
 - gi No. 1078797
 - % Identity 80.2
 - Alignment Length 96
 - Location of Alignment in SEQ ID NO 2192: from 1 to 96
 - Alignment No. 14223
 - gi No. 1170767
 - % Identity 75
 - Alignment Length 96
 - Location of Alignment in SEQ ID NO 2192: from 1 to 96
 - Alignment No. 14224
 - gi No. 1262435
 - % Identity 81.3
 - Alignment Length 96
 - Location of Alignment in SEQ ID NO 2192: from 1 to 96
 - Alignment No. 14225
 - gi No. 1346812
 - % Identity 81.3
 - Alignment Length 96

- Location of Alignment in SEQ ID NO 2192: from 1 to 96
- Alignment No. 14226
- gi No. 1709799
- % Identity 81.3
- Alignment Length 96
- Location of Alignment in SEQ ID NO 2192: from 1 to 96
- Alignment No. 14227
- gi No. 1709800
- % Identity 81.3
- Alignment Length 96
- Location of Alignment in SEQ ID NO 2192: from 1 to 96
- Alignment No. 14228
- gi No. 228885
- % Identity 70.3
- Alignment Length 91
- Location of Alignment in SEQ ID NO 2192: from 1 to 91
- Alignment No. 14229
- gi No. 2492521
- % Identity 76
- Alignment Length 96
- Location of Alignment in SEQ ID NO 2192: from 1 to 96
- Alignment No. 14230
- gi No. 2564007
- % Identity 81.3
- Alignment Length 96
- Location of Alignment in SEQ ID NO 2192: from 1 to 96
- Alignment No. 14231
- gi No. 2661071
- % Identity 81.3
- Alignment Length 96
- Location of Alignment in SEQ ID NO 2192: from 1 to 96
- Alignment No. 14232
- gi No. 2815905
- % Identity 81.3
- Alignment Length 96
- Location of Alignment in SEQ ID NO 2192: from 1 to 96
- Alignment No. 14233
- gi No. 2982331
- % Identity 94.8
- Alignment Length 96
- Location of Alignment in SEQ ID NO 2192: from 1 to 96
- Alignment No. 14234
- gi No. 3041724
- % Identity 81.3
- Alignment Length 96
- Location of Alignment in SEQ ID NO 2192: from 1 to 96
- Alignment No. 14235
- gi No. 3122626
- % Identity 81.3
- Alignment Length 96
- Location of Alignment in SEQ ID NO 2192: from 1 to 96

- Alignment No. 14236
- gi No. 3790757
- % Identity 77.1
- Alignment Length 96
- Location of Alignment in SEQ ID NO 2192: from 1 to 96
- Alignment No. 14237
- gi No. 3979998
- % Identity 78.1
- Alignment Length 96
- Location of Alignment in SEQ ID NO 2192: from 1 to 96
- Alignment No. 14238
- gi No. 4506213
- % Identity 81.3
- Alignment Length 96
- Location of Alignment in SEQ ID NO 2192: from 1 to 96
- Alignment No. 14239
- gi No. 464863
- % Identity 81.3
- Alignment Length 96
- Location of Alignment in SEQ ID NO 2192: from 1 to 96
- (B) Polypeptide Sequence
 - Pat. Appln. SEQ ID NO 2193
 - Ceres seq_id 1502529
 - Location of start within SEQ ID NO 2191: at 76 nt.
- (C) Nomination and Annotation of Domains within Predicted Polypeptide(s)
 - (D) Related Amino Acid Sequences
 - Alignment No. 14240
 - gi No. 1078797
 - % Identity 80.2
 - Alignment Length 96
 - Location of Alignment in SEQ ID NO 2193: from 1 to 71
 - Alignment No. 14241
 - gi No. 1170767
 - % Identity 75
 - Alignment Length 96
 - Location of Alignment in SEQ ID NO 2193: from 1 to 71
 - Alignment No. 14242
 - gi No. 1262435
 - % Identity 81.3
 - Alignment Length 96
 - Location of Alignment in SEQ ID NO 2193: from 1 to 71
 - Alignment No. 14243
 - gi No. 1346812
 - % Identity 81.3
 - Alignment Length 96
 - Location of Alignment in SEQ ID NO 2193: from 1 to 71
 - Alignment No. 14244
 - gi No. 1709799
 - % Identity 81.3
 - Alignment Length 96

- Location of Alignment in SEQ ID NO 2193: from 1 to 71
- Alignment No. 14245
- gi No. 1709800
- % Identity 81.3
- Alignment Length 96
- Location of Alignment in SEQ ID NO 2193: from 1 to 71
- Alignment No. 14246
- gi No. 228885
- % Identity 70.3
- Alignment Length 91
- Location of Alignment in SEQ ID NO 2193: from 1 to 66
- Alignment No. 14247
- gi No. 2492521
- % Identity 76
- Alignment Length 96
- Location of Alignment in SEQ ID NO 2193: from 1 to 71
- Alignment No. 14248
- gi No. 2564007
- % Identity 81.3
- Alignment Length 96
- Location of Alignment in SEQ ID NO 2193: from 1 to 71
- Alignment No. 14249
- gi No. 2661071
- % Identity 81.3
- Alignment Length 96
- Location of Alignment in SEQ ID NO 2193: from 1 to 71
- Alignment No. 14250
- gi No. 2815905
- % Identity 81.3
- Alignment Length 96
- Location of Alignment in SEQ ID NO 2193: from 1 to 71
- Alignment No. 14251
- gi No. 2982331
- % Identity 94.8
- Alignment Length 96
- Location of Alignment in SEQ ID NO 2193: from 1 to 71
- Alignment No. 14252
- gi No. 3041724
- % Identity 81.3
- Alignment Length 96
- Location of Alignment in SEQ ID NO 2193: from 1 to 71
- Alignment No. 14253
- gi No. 3122626
- % Identity 81.3
- Alignment Length 96
- Location of Alignment in SEQ ID NO 2193: from 1 to 71
- Alignment No. 14254
- gi No. 3790757
- % Identity 77.1
- Alignment Length 96
- Location of Alignment in SEQ ID NO 2193: from 1 to 71

- Alignment No. 14255
- gi No. 3979998
- % Identity 78.1
- Alignment Length 96
- Location of Alignment in SEQ ID NO 2193: from 1 to 71
- Alignment No. 14256
- gi No. 4506213
- % Identity 81.3
- Alignment Length 96
- Location of Alignment in SEQ ID NO 2193: from 1 to 71
- Alignment No. 14257
- gi No. 464863
- % Identity 81.3
- Alignment Length 96
- Location of Alignment in SEQ ID NO 2193: from 1 to 71
- (B) Polypeptide Sequence
 - Pat. Appln. SEQ ID NO 2194
 - Ceres seq_id 1502530
 - Location of start within SEQ ID NO 2191: at 85 nt.
- - (D) Related Amino Acid Sequences
 - Alignment No. 14258
 - gi No. 1078797
 - % Identity 80.2
 - Alignment Length 96
 - Location of Alignment in SEQ ID NO 2194: from 1 to 68
 - Alignment No. 14259
 - gi No. 1170767
 - % Identity 75
 - Alignment Length 96
 - Location of Alignment in SEQ ID NO 2194: from 1 to 68
 - Alignment No. 14260
 - gi No. 1262435
 - % Identity 81.3
 - Alignment Length 96
 - Location of Alignment in SEQ ID NO 2194: from 1 to 68
 - Alignment No. 14261
 - gi No. 1346812
 - % Identity 81.3
 - Alignment Length 96
 - Location of Alignment in SEQ ID NO 2194: from 1 to 68
 - Alignment No. 14262
 - gi No. 1709799
 - % Identity 81.3
 - Alignment Length 96
 - Location of Alignment in SEQ ID NO 2194: from 1 to 68
 - Alignment No. 14263
 - gi No. 1709800
 - % Identity 81.3
 - Alignment Length 96



- Location of Alignment in SEQ ID NO 2194: from 1 to 68
- Alignment No. 14264
- gi No. 228885
- % Identity 70.3
- Alignment Length 91
- Location of Alignment in SEQ ID NO 2194: from 1 to 63
- Alignment No. 14265
- gi No. 2492521
- % Identity 76
- Alignment Length 96
- Location of Alignment in SEQ ID NO 2194: from 1 to 68
- Alignment No. 14266
- gi No. 2564007
- % Identity 81.3
- Alignment Length 96
- Location of Alignment in SEQ ID NO 2194: from 1 to 68
- Alignment No. 14267
- gi No. 2661071
- % Identity 81.3
- Alignment Length 96
- Location of Alignment in SEQ ID NO 2194: from 1 to 68
- Alignment No. 14268
- gi No. 2815905
- % Identity 81.3
- Alignment Length 96
- Location of Alignment in SEQ ID NO 2194: from 1 to 68
- Alignment No. 14269
- gi No. 2982331
- % Identity 94.8
- Alignment Length 96
- Location of Alignment in SEQ ID NO 2194: from 1 to 68
- Alignment No. 14270
- gi No. 3041724
- % Identity 81.3
- Alignment Length 96
- Location of Alignment in SEQ ID NO 2194: from 1 to 68
- Alignment No. 14271
- gi No. 3122626
- % Identity 81.3
- Alignment Length 96
- Location of Alignment in SEQ ID NO 2194: from 1 to 68
- Alignment No. 14272
- gi No. 3790757
- % Identity 77.1
- Alignment Length 96
- Location of Alignment in SEQ ID NO 2194: from 1 to 68
- Alignment No. 14273
- gi No. 3979998
- % Identity 78.1
- Alignment Length 96
- Location of Alignment in SEQ ID NO 2194: from 1 to 68

- Alignment No. 14274
- gi No. 4506213
- % Identity 81.3
- Alignment Length 96
- Location of Alignment in SEQ ID NO 2194: from 1 to 68
- Alignment No. 14275
- gi No. 464863
- % Identity 81.3
- Alignment Length 96
- Location of Alignment in SEQ ID NO 2194: from 1 to 68

- (A) Polynucleotide Sequence
 - Pat. Appln. SEQ ID NO 2195
 - Ceres seq_id 1502542
 - (B) Polypeptide Sequence
 - Pat. Appln. SEQ ID NO 2196
 - Ceres seq_id 1502543
 - Location of start within SEQ ID NO 2195: at 1 nt.
- - Alignment No. 14276
 - Ras family
 - Location within SEQ ID NO 2196: from 69 to 147 aa.
 - Alignment No. 14277
 - ADP-ribosylation factor family
 - Location within SEQ ID NO 2196: from 52 to 169 aa.
 - Alignment No. 14278
 - G-protein alpha subunit
 - Location within SEQ ID NO 2196: from 94 to 169 aa.
 - (D) Related Amino Acid Sequences
 - Alignment No. 14279
 - gi No. 1065361
 - % Identity 90.8
 - Alignment Length 119
 - Location of Alignment in SEQ ID NO 2196: from 52 to 169
 - Alignment No. 14280
 - qi No. 114121
 - % Identity 79
 - Alignment Length 119
 - Location of Alignment in SEQ ID NO 2196: from 51 to 169
 - Alignment No. 14281
 - gi No. 114122
 - % Identity 91.7
 - Alignment Length 120
 - Location of Alignment in SEQ ID NO 2196: from 51 to 169
 - Alignment No. 14282
 - gi No. 114124
 - % Identity 78.3
 - Alignment Length 120
 - Location of Alignment in SEQ ID NO 2196: from 51 to 169

- Alignment No. 14283
- gi No. 114128
- % Identity 74.8
- Alignment Length 115
- Location of Alignment in SEQ ID NO 2196: from 56 to 169
- Alignment No. 14284
- gi No. 114131
- % Identity 74.4
- Alignment Length 121
- Location of Alignment in SEQ ID NO 2196: from 51 to 169
- Alignment No. 14285
- gi No. 1168489
- % Identity 85
- Alignment Length 120
- Location of Alignment in SEQ ID NO 2196: from 51 to 169
- Alignment No. 14286
- gi No. 1351973
- % Identity 86.7
- Alignment Length 120
- Location of Alignment in SEQ ID NO 2196: from 51 to 169
- Alignment No. 14287
- gi No. 1351974
- % Identity 97.5
- Alignment Length 120
- Location of Alignment in SEQ ID NO 2196: from 51 to 169
- Alignment No. 14288
- gi No. 1703373
- % Identity 90.8
- Alignment Length 120
- Location of Alignment in SEQ ID NO 2196: from 51 to 169
- Alignment No. 14289
- gi No. 1703374
- % Identity 95.8
- Alignment Length 120
- Location of Alignment in SEQ ID NO 2196: from 51 to 169
- Alignment No. 14290
- qi No. 1703375
- % Identity 98.3
- Alignment Length 120
- Location of Alignment in SEQ ID NO 2196: from 51 to 169
- Alignment No. 14291
- gi No. 1703376
- % Identity 93.3
- Alignment Length 120
- Location of Alignment in SEQ ID NO 2196: from 51 to 169
- Alignment No. 14292
- gi No. 1703377
- % Identity 90.8
- Alignment Length 120
- Location of Alignment in SEQ ID NO 2196: from 51 to 169
- Alignment No. 14293

- gi No. 1703378
- % Identity 88.3
- Alignment Length 120
- Location of Alignment in SEQ ID NO 2196: from 51 to 169
- Alignment No. 14294
- gi No. 1703379

- % Identity 75.7

- Alignment Length 115Location of Alignment in SEQ ID NO 2196: from 56 to 169
- Alignment No. 14295 - gi No. 1703380 - % Identity 98.3
- Alignment Length 120
- Location of Alignment in SEQ ID NO 2196: from 51 to 169
- Alignment No. 14296 - gi No. 2129946 - % Identity 97.7 - Alignment Length 87
- Location of Alignment in SEQ ID NO 2196: from 51 to 137
- Alignment No. 14297 - gi No. 2293566 - % Identity 98.3 - Alignment Length 120
- Location of Alignment in SEQ ID NO 2196: from 51 to 169
- Alignment No. 14298 - gi No. 2462736 - % Identity 97.6 - Alignment Length 42
- Location of Alignment in SEQ ID NO 2196: from 51 to 92
- Alignment No. 14299
- gi No. 2492925
- % Identity 80
- Alignment Length 120
- Location of Alignment in SEQ ID NO 2196: from 51 to 169
- Alignment No. 14300
- gi No. 2689631
- % Identity 98.3
- Alignment Length 120
- Location of Alignment in SEQ ID NO 2196: from 51 to 169
- Alignment No. 14301
- gi No. 283391
- % Identity 85
- Alignment Length 120
- Location of Alignment in SEQ ID NO 2196: from 51 to 169
- Alignment No. 14302
- gi No. 2852443
- % Identity 95
- Alignment Length 120
- Location of Alignment in SEQ ID NO 2196: from 51 to 169
- Alignment No. 14303
- gi No. 2854182

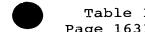
- % Identity 87.4
- Alignment Length 119
- Location of Alignment in SEQ ID NO 2196: from 51 to 169
- Alignment No. 14304
- gi No. 3182915
- % Identity 90.8
- Alignment Length 120
- Location of Alignment in SEQ ID NO 2196: from 51 to 169
- Alignment No. 14305
- gi No. 3182916
- % Identity 80.8
- Alignment Length 120
- Location of Alignment in SEQ ID NO 2196: from 51 to 169
- Alignment No. 14306
- gi No. 3182917
- % Identity 90.8
- Alignment Length 120
- Location of Alignment in SEQ ID NO 2196: from 51 to 169
- Alignment No. 14307
- gi No. 3182919
- % Identity 95.8
- Alignment Length 120
- Location of Alignment in SEQ ID NO 2196: from 51 to 169
- Alignment No. 14308
- gi No. 3252999
- % Identity 94.6
- Alignment Length 93
- Location of Alignment in SEQ ID NO 2196: from 68 to 160
- Alignment No. 14309
- gi No. 3746799
- % Identity 87.3
- Alignment Length 102
- Location of Alignment in SEQ ID NO 2196: from 69 to 169
- Alignment No. 14310
- gi No. 3746801
- % Identity 86.3
- Alignment Length 102
- Location of Alignment in SEQ ID NO 2196: from 69 to 169
- Alignment No. 14311
- gi No. 4056469
- % Identity 98.3
- Alignment Length 120
- Location of Alignment in SEQ ID NO 2196: from 51 to 169
- Alignment No. 14312
- qi No. 4102193
- % Identity 77.3
- Alignment Length 66
- Location of Alignment in SEQ ID NO 2196: from 51 to 116
- Alignment No. 14313
- gi No. 4324967
- % Identity 98.3

- Alignment Length 117
- Location of Alignment in SEQ ID NO 2196: from 54 to 169
- Alignment No. 14314
- qi No. 4502201
- % Identity 90.8
- Alignment Length 120
- Location of Alignment in SEQ ID NO 2196: from 51 to 169
- Alignment No. 14315
- gi No. 4502203
- % Identity 90
- Alignment Length 120
- Location of Alignment in SEQ ID NO 2196: from 51 to 169
- Alignment No. 14316
- gi No. 4502205
- % Identity 85.8
- Alignment Length 120
- Location of Alignment in SEQ ID NO 2196: from 51 to 169
- Alignment No. 14317
- gi No. 4502209
- % Identity 88.3
- Alignment Length 120
- Location of Alignment in SEQ ID NO 2196: from 51 to 169
- Alignment No. 14318
- gi No. 4502211
- % Identity 74.8
- Alignment Length 115
- Location of Alignment in SEQ ID NO 2196: from 56 to 169
- Alignment No. 14319
- gi No. 461532
- % Identity 89.2
- Alignment Length 120
- Location of Alignment in SEQ ID NO 2196: from 51 to 169
- Alignment No. 14320
- gi No. 461533
- % Identity 89.2
- Alignment Length 120
- Location of Alignment in SEQ ID NO 2196: from 51 to 169
- Alignment No. 14321
- gi No. 4662630
- % Identity 70.6
- Alignment Length 119
- Location of Alignment in SEQ ID NO 2196: from 51 to 169
- Alignment No. 14322
- gi No. 543841
- % Identity 99.2
- Alignment Length 120
- Location of Alignment in SEQ ID NO 2196: from 51 to 169
- Alignment No. 14323
- gi No. 543842
- % Identity 90
- Alignment Length 120



- Location of Alignment in SEQ ID NO 2196: from 51 to 169
- Alignment No. 14324
- gi No. 543843
- % Identity 88.3
- Alignment Length 120
- Location of Alignment in SEQ ID NO 2196: from 51 to 169
- Alignment No. 14325
- gi No. 543844
- % Identity 85.8
- Alignment Length 120
- Location of Alignment in SEQ ID NO 2196: from 51 to 169
- Alignment No. 14326
- gi No. 5579053
- % Identity 70.7
- Alignment Length 123
- Location of Alignment in SEQ ID NO 2196: from 48 to 169
- Alignment No. 14327
- qi No. 728881
- % Identity 85.8
- Alignment Length 120
- Location of Alignment in SEQ ID NO 2196: from 51 to 169
- Alignment No. 14328
- gi No. 728883
- % Identity 74.8
- Alignment Length 115
- Location of Alignment in SEQ ID NO 2196: from 56 to 169
- Alignment No. 14329
- gi No. 83900
- % Identity 85
- Alignment Length 120
- Location of Alignment in SEQ ID NO 2196: from 51 to 169
- (B) Polypeptide Sequence
 - Pat. Appln. SEQ ID NO 2197
 - Ceres seg id 1502544
 - Location of start within SEQ ID NO 2195: at 151 nt.
- - Alignment No. 14330
 - Ras family
 - Location within SEQ ID NO 2197: from 19 to 97 aa.
 - Alignment No. 14331
 - ADP-ribosylation factor family
 - Location within SEQ ID NO 2197: from 2 to 119 aa.
 - Alignment No. 14332
 - G-protein alpha subunit
 - Location within SEQ ID NO 2197: from 44 to 119 aa.
 - (D) Related Amino Acid Sequences
 - Alignment No. 14333
 - gi No. 1065361
 - % Identity 90.8

- Alignment Length 119
- Location of Alignment in SEQ ID NO 2197: from 2 to 119
- Alignment No. 14334
- gi No. 114121
- % Identity 79
- Alignment Length 119
- Location of Alignment in SEQ ID NO 2197: from 1 to 119
- Alignment No. 14335
- gi No. 114122
- % Identity 91.7
- Alignment Length 120
- Location of Alignment in SEQ ID NO 2197: from 1 to 119
- Alignment No. 14336
- qi No. 114124
- % Identity 78.3
- Alignment Length 120
- Location of Alignment in SEQ ID NO 2197: from 1 to 119
- Alignment No. 14337
- gi No. 114128
- % Identity 74.8
- Alignment Length 115
- Location of Alignment in SEQ ID NO 2197: from 6 to 119
- Alignment No. 14338
- gi No. 114131
- % Identity 74.4
- Alignment Length 121
- Location of Alignment in SEQ ID NO 2197: from 1 to 119
- Alignment No. 14339
- gi No. 1168489
- % Identity 85
- Alignment Length 120
- Location of Alignment in SEQ ID NO 2197: from 1 to 119
- Alignment No. 14340
- gi No. 1351973
- % Identity 86.7
- Alignment Length 120
- Location of Alignment in SEQ ID NO 2197: from 1 to 119
- Alignment No. 14341
- gi No. 1351974
- % Identity 97.5
- Alignment Length 120
- Location of Alignment in SEQ ID NO 2197: from 1 to 119
- Alignment No. 14342
- gi No. 1703373
- % Identity 90.8
- Alignment Length 120
- Location of Alignment in SEQ ID NO 2197: from 1 to 119
- Alignment No. 14343
- gi No. 1703374
- % Identity 95.8
- Alignment Length 120



- Location of Alignment in SEQ ID NO 2197: from 1 to 119
- Alignment No. 14344
- gi No. 1703375
- % Identity 98.3
- Alignment Length 120
- Location of Alignment in SEQ ID NO 2197: from 1 to 119
- Alignment No. 14345
- gi No. 1703376
- % Identity 93.3
- Alignment Length 120
- Location of Alignment in SEQ ID NO 2197: from 1 to 119
- Alignment No. 14346
- gi No. 1703377
- % Identity 90.8
- Alignment Length 120
- Location of Alignment in SEQ ID NO 2197: from 1 to 119
- Alignment No. 14347
- gi No. 1703378
- % Identity 88.3
- Alignment Length 120
- Location of Alignment in SEQ ID NO 2197: from 1 to 119
- Alignment No. 14348
- gi No. 1703379
- % Identity 75.7
- Alignment Length 115
- Location of Alignment in SEQ ID NO 2197: from 6 to 119
- Alignment No. 14349
- gi No. 1703380
- % Identity 98.3
- Alignment Length 120
- Location of Alignment in SEQ ID NO 2197: from 1 to 119
- Alignment No. 14350
- gi No. 2129946
- % Identity 97.7
- Alignment Length 87
- Location of Alignment in SEQ ID NO 2197: from 1 to 87
- Alignment No. 14351
- gi No. 2293566
- % Identity 98.3
- Alignment Length 120
- Location of Alignment in SEQ ID NO 2197: from 1 to 119
- Alignment No. 14352
- gi No. 2462736
- % Identity 97.6
- Alignment Length 42
- Location of Alignment in SEQ ID NO 2197: from 1 to 42
- Alignment No. 14353
- gi No. 2492925
- % Identity 80
- Alignment Length 120
- Location of Alignment in SEQ ID NO 2197: from 1 to 119

- Alignment No. 14354
- gi No. 2689631
- % Identity 98.3
- Alignment Length 120
- Location of Alignment in SEQ ID NO 2197: from 1 to 119
- Alignment No. 14355
- gi No. 283391
- % Identity 85
- Alignment Length 120
- Location of Alignment in SEQ ID NO 2197: from 1 to 119
- Alignment No. 14356
- gi No. 2852443
- % Identity 95
- Alignment Length 120
- Location of Alignment in SEQ ID NO 2197: from 1 to 119
- Alignment No. 14357
- gi No. 2854182
- % Identity 87.4
- Alignment Length 119
- Location of Alignment in SEQ ID NO 2197: from 1 to 119
- Alignment No. 14358
- gi No. 3182915
- % Identity 90.8
- Alignment Length 120
- Location of Alignment in SEQ ID NO 2197: from 1 to 119
- Alignment No. 14359
- gi No. 3182916
- % Identity 80.8
- Alignment Length 120
- Location of Alignment in SEQ ID NO 2197: from 1 to 119
- Alignment No. 14360
- qi No. 3182917
- % Identity 90.8
- Alignment Length 120
- Location of Alignment in SEQ ID NO 2197: from 1 to 119
- Alignment No. 14361
- gi No. 3182919
- % Identity 95.8
- Alignment Length 120
- Location of Alignment in SEQ ID NO 2197: from 1 to 119
- Alignment No. 14362
- gi No. 3252999
- % Identity 94.6
- Alignment Length 93
- Location of Alignment in SEQ ID NO 2197: from 18 to 110
- Alignment No. 14363
- gi No. 3746799
- % Identity 87.3
- Alignment Length 102
- Location of Alignment in SEQ ID NO 2197: from 19 to 119

- Alignment No. 14364
- gi No. 3746801
- % Identity 86.3
- Alignment Length 102
- Location of Alignment in SEQ ID NO 2197: from 19 to 119
- Alignment No. 14365
- gi No. 4056469
- % Identity 98.3
- Alignment Length 120
- Location of Alignment in SEQ ID NO 2197: from 1 to 119
- Alignment No. 14366
- gi No. 4102193
- % Identity 77.3
- Alignment Length 66
- Location of Alignment in SEQ ID NO 2197: from 1 to 66
- Alignment No. 14367
- gi No. 4324967
- % Identity 98.3
- Alignment Length 117
- Location of Alignment in SEQ ID NO 2197: from 4 to 119
- Alignment No. 14368
- gi No. 4502201
- % Identity 90.8
- Alignment Length 120
- Location of Alignment in SEQ ID NO 2197: from 1 to 119
- Alignment No. 14369
- gi No. 4502203
- % Identity 90
- Alignment Length 120
- Location of Alignment in SEQ ID NO 2197: from 1 to 119
- Alignment No. 14370
- gi No. 4502205
- % Identity 85.8
- Alignment Length 120
- Location of Alignment in SEQ ID NO 2197: from 1 to 119
- Alignment No. 14371
- gi No. 4502209
- % Identity 88.3
- Alignment Length 120
- Location of Alignment in SEQ ID NO 2197: from 1 to 119
- Alignment No. 14372
- gi No. 4502211
- % Identity 74.8
- Alignment Length 115
- Location of Alignment in SEQ ID NO 2197: from 6 to 119
- Alignment No. 14373
- gi No. 461532
- % Identity 89.2
- Alignment Length 120
- Location of Alignment in SEQ ID NO 2197: from 1 to 119
- Alignment No. 14374

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- gi No. 461533
- % Identity 89.2
- Alignment Length 120
- Location of Alignment in SEQ ID NO 2197: from 1 to 119
- Alignment No. 14375
- qi No. 4662630
- % Identity 70.6
- Alignment Length 119
- Location of Alignment in SEQ ID NO 2197: from 1 to 119
- Alignment No. 14376
- gi No. 543841
- % Identity 99.2
- Alignment Length 120
- Location of Alignment in SEQ ID NO 2197: from 1 to 119
- Alignment No. 14377
- gi No. 543842
- % Identity 90
- Alignment Length 120
- Location of Alignment in SEQ ID NO 2197: from 1 to 119
- Alignment No. 14378
- gi No. 543843
- % Identity 88.3
- Alignment Length 120
- Location of Alignment in SEQ ID NO 2197: from 1 to 119
- Alignment No. 14379
- gi No. 543844
- % Identity 85.8
- Alignment Length 120
- Location of Alignment in SEQ ID NO 2197: from 1 to 119
- Alignment No. 14380
- gi No. 5579053
- % Identity 70.7
- Alignment Length 123
- Location of Alignment in SEQ ID NO 2197: from 1 to 119
- Alignment No. 14381
- gi No. 728881
- % Identity 85.8
- Alignment Length 120
- Location of Alignment in SEQ ID NO 2197: from 1 to 119
- Alignment No. 14382
- gi No. 728883
- % Identity 74.8
- Alignment Length 115
- Location of Alignment in SEQ ID NO 2197: from 6 to 119
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- Location of Alignment in SEQ ID NO 2197: from 1 to 119

- Alignment No. 14383

- Alignment Length 120

- gi No. 83900
- % Identity 85

- Ceres seg id 1502545
- Location of start within SEQ ID NO 2195: at 202 nt.
- (C) Nomination and Annotation of Domains within Predicted Polypeptide(s)
 - Alignment No. 14384
 - Ras family
 - Location within SEQ ID NO 2198: from 2 to 80 aa.
 - Alignment No. 14385
 - ADP-ribosylation factor family
 - Location within SEQ ID NO 2198: from 1 to 102 aa.
 - Alignment No. 14386
 - G-protein alpha subunit
 - Location within SEQ ID NO 2198: from 27 to 102 aa.
 - (D) Related Amino Acid Sequences
 - Alignment No. 14387
 - gi No. 1065361
 - % Identity 90.8
 - Alignment Length 119
 - Location of Alignment in SEQ ID NO 2198: from 1 to 102
 - Alignment No. 14388
 - gi No. 114121
 - % Identity 79
 - Alignment Length 119
 - Location of Alignment in SEQ ID NO 2198: from 1 to 102
 - Alignment No. 14389
 - gi No. 114122
 - % Identity 91.7
 - Alignment Length 120
 - Location of Alignment in SEQ ID NO 2198: from 1 to 102
 - Alignment No. 14390
 - gi No. 114124
 - % Identity 78.3
 - Alignment Length 120
 - Location of Alignment in SEQ ID NO 2198: from 1 to 102
 - Alignment No. 14391
 - gi No. 114128
 - % Identity 74.8
 - Alignment Length 115
 - Location of Alignment in SEQ ID NO 2198: from 1 to 102
 - Alignment No. 14392
 - gi No. 114131
 - % Identity 74.4
 - Alignment Length 121
 - Location of Alignment in SEQ ID NO 2198: from 1 to 102
 - Alignment No. 14393
 - gi No. 1168489
 - % Identity 85
 - Alignment Length 120
 - Location of Alignment in SEQ ID NO 2198: from 1 to 102
 - Alignment No. 14394

- gi No. 1351973
- % Identity 86.7
- Alignment Length 120
- Location of Alignment in SEQ ID NO 2198: from 1 to 102
- Alignment No. 14395
- gi No. 1351974
- % Identity 97.5
- Alignment Length 120
- Location of Alignment in SEQ ID NO 2198: from 1 to 102
- Alignment No. 14396
- gi No. 1703373
- % Identity 90.8
- Alignment Length 120
- Location of Alignment in SEQ ID NO 2198: from 1 to 102
- Alignment No. 14397
- gi No. 1703374
- % Identity 95.8
- Alignment Length 120
- Location of Alignment in SEQ ID NO 2198: from 1 to 102
- Alignment No. 14398
- gi No. 1703375
- % Identity 98.3
- Alignment Length 120
- Location of Alignment in SEQ ID NO 2198: from 1 to 102
- Alignment No. 14399
- gi No. 1703376
- % Identity 93.3
- Alignment Length 120
- Location of Alignment in SEQ ID NO 2198: from 1 to 102
- Alignment No. 14400
- gi No. 1703377
- % Identity 90.8
- Alignment Length 120
- Location of Alignment in SEQ ID NO 2198: from 1 to 102
- Alignment No. 14401
- gi No. 1703378
- % Identity 88.3
- Alignment Length 120
- Location of Alignment in SEQ ID NO 2198: from 1 to 102
- Alignment No. 14402
- gi No. 1703379
- % Identity 75.7
- Alignment Length 115
- Location of Alignment in SEQ ID NO 2198: from 1 to 102
- Alignment No. 14403
- gi No. 1703380
- % Identity 98.3
- Alignment Length 120
- Location of Alignment in SEQ ID NO 2198: from 1 to 102
- Alignment No. 14404
- gi No. 2129946

- % Identity 97.7
- Alignment Length 87
- Location of Alignment in SEQ ID NO 2198: from 1 to 70
- Alignment No. 14405
- gi No. 2293566
- % Identity 98.3
- Alignment Length 120
- Location of Alignment in SEQ ID NO 2198: from 1 to 102
- Alignment No. 14406
- gi No. 2462736
- % Identity 97.6
- Alignment Length 42
- Location of Alignment in SEQ ID NO 2198: from 1 to 25
- Alignment No. 14407
- qi No. 2492925
- % Identity 80
- Alignment Length 120
- Location of Alignment in SEQ ID NO 2198: from 1 to 102
- Alignment No. 14408
- gi No. 2689631
- % Identity 98.3
- Alignment Length 120
- Location of Alignment in SEQ ID NO 2198: from 1 to 102
- Alignment No. 14409
- gi No. 283391
- % Identity 85
- Alignment Length 120
- Location of Alignment in SEQ ID NO 2198: from 1 to 102 $\,$
- Alignment No. 14410
- gi No. 2852443
- % Identity 95
- Alignment Length 120
- Location of Alignment in SEQ ID NO 2198: from 1 to 102
- Alignment No. 14411
- gi No. 2854182
- % Identity 87.4
- Alignment Length 119
- Location of Alignment in SEQ ID NO 2198: from 1 to 102
- Alignment No. 14412
- gi No. 3182915
- % Identity 90.8
- Alignment Length 120
- Location of Alignment in SEQ ID NO 2198: from 1 to 102
- Alignment No. 14413
- gi No. 3182916
- % Identity 80.8
- Alignment Length 120
- Location of Alignment in SEQ ID NO 2198: from 1 to 102
- Alignment No. 14414
- gi No. 3182917
- % Identity 90.8

- Alignment Length 120
- Location of Alignment in SEQ ID NO 2198: from 1 to 102
- Alignment No. 14415
- gi No. 3182919
- % Identity 95.8
- Alignment Length 120
- Location of Alignment in SEQ ID NO 2198: from 1 to 102
- Alignment No. 14416
- gi No. 3252999
- % Identity 94.6
- Alignment Length 93
- Location of Alignment in SEQ ID NO 2198: from 1 to 93
- Alignment No. 14417
- gi No. 3746799
- % Identity 87.3
- Alignment Length 102
- Location of Alignment in SEQ ID NO 2198: from 2 to 102
- Alignment No. 14418
- gi No. 3746801
- % Identity 86.3
- Alignment Length 102
- Location of Alignment in SEQ ID NO 2198: from 2 to 102
- Alignment No. 14419
- gi No. 4056469
- % Identity 98.3
- Alignment Length 120
- Location of Alignment in SEQ ID NO 2198: from 1 to 102
- Alignment No. 14420
- gi No. 4102193
- % Identity 77.3
- Alignment Length 66
- Location of Alignment in SEQ ID NO 2198: from 1 to 49
- Alignment No. 14421
- qi No. 4324967
- % Identity 98.3
- Alignment Length 117
- Location of Alignment in SEQ ID NO 2198: from 1 to 102
- Alignment No. 14422
- gi No. 4502201
- % Identity 90.8
- Alignment Length 120
- Location of Alignment in SEQ ID NO 2198: from 1 to 102
- Alignment No. 14423
- gi No. 4502203
- % Identity 90
- Alignment Length 120
- Location of Alignment in SEQ ID NO 2198: from 1 to 102
- Alignment No. 14424
- gi No. 4502205
- % Identity 85.8
- Alignment Length 120

- Location of Alignment in SEQ ID NO 2198: from 1 to 102
- Alignment No. 14425
- gi No. 4502209
- % Identity 88.3
- Alignment Length 120
- Location of Alignment in SEQ ID NO 2198: from 1 to 102
- Alignment No. 14426
- gi No. 4502211
- % Identity 74.8
- Alignment Length 115
- Location of Alignment in SEQ ID NO 2198: from 1 to 102
- Alignment No. 14427
- gi No. 461532
- % Identity 89.2
- Alignment Length 120
- Location of Alignment in SEQ ID NO 2198: from 1 to 102
- Alignment No. 14428
- gi No. 461533
- % Identity 89.2
- Alignment Length 120
- Location of Alignment in SEQ ID NO 2198: from 1 to 102
- Alignment No. 14429
- gi No. 4662630
- % Identity 70.6
- Alignment Length 119
- Location of Alignment in SEQ ID NO 2198: from 1 to 102
- Alignment No. 14430
- gi No. 543841
- % Identity 99.2
- Alignment Length 120
- Location of Alignment in SEQ ID NO 2198: from 1 to 102
- Alignment No. 14431
- gi No. 543842
- % Identity 90
- Alignment Length 120
- Location of Alignment in SEQ ID NO 2198: from 1 to 102
- Alignment No. 14432
- qi No. 543843
- % Identity 88.3
- Alignment Length 120
- Location of Alignment in SEQ ID NO 2198: from 1 to 102
- Alignment No. 14433
- gi No. 543844
- % Identity 85.8
- Alignment Length 120
- Location of Alignment in SEQ ID NO 2198: from 1 to 102
- Alignment No. 14434
- gi No. 5579053
- % Identity 70.7
- Alignment Length 123
- Location of Alignment in SEQ ID NO 2198: from 1 to 102

- Alignment No. 14435
- gi No. 728881
- % Identity 85.8
- Alignment Length 120
- Location of Alignment in SEQ ID NO 2198: from 1 to 102
- Alignment No. 14436
- gi No. 728883
- % Identity 74.8
- Alignment Length 115
- Location of Alignment in SEQ ID NO 2198: from 1 to 102
- Alignment No. 14437
- gi No. 83900
- % Identity 85
- Alignment Length 120
- Location of Alignment in SEQ ID NO 2198: from 1 to 102

- (A) Polynucleotide Sequence
 - Pat. Appln. SEQ ID NO 2199
 - Ceres seq_id 1502573
 - (B) Polypeptide Sequence
 - Pat. Appln. SEQ ID NO 2200
 - Ceres seq_id 1502574
 - Location of start within SEQ ID NO 2199: at 1 nt.
- - (D) Related Amino Acid Sequences
 - Alignment No. 14438
 - qi No. 3935181
 - % Identity 82.7
 - Alignment Length 75
 - Location of Alignment in SEQ ID NO 2200: from 9 to 83
 - (B) Polypeptide Sequence
 - Pat. Appln. SEQ ID NO 2201
 - Ceres seq_id 1502575
 - Location of start within SEQ ID NO 2199: at 2 nt.
- - (D) Related Amino Acid Sequences
 - (B) Polypeptide Sequence
 - Pat. Appln. SEQ ID NO 2202
 - Ceres seq_id 1502576
 - Location of start within SEQ ID NO 2199: at 3 nt.
- (C) Nomination and Annotation of Domains within Predicted Polypeptide(s)
 - (D) Related Amino Acid Sequences
 - Alignment No. 14439
 - gi No. 3935181
 - % Identity 71.7
 - Alignment Length 113
 - Location of Alignment in SEQ ID NO 2202: from 50 to 161

- (A) Polynucleotide Sequence
 - Pat. Appln. SEQ ID NO 2203
 - Ceres seq_id 1502613
 - (B) Polypeptide Sequence
 - Pat. Appln. SEQ ID NO 2204
 - Ceres seq_id 1502614
 - Location of start within SEQ ID NO 2203: at 1 nt.
- - (D) Related Amino Acid Sequences
 - (B) Polypeptide Sequence
 - Pat. Appln. SEQ ID NO 2205
 - Ceres seq_id 1502615
 - Location of start within SEQ ID NO 2203: at 2 nt.
- - (D) Related Amino Acid Sequences
 - Alignment No. 14440
 - gi No. 3023243
 - % Identity 71.4
 - Alignment Length 14
 - Location of Alignment in SEQ ID NO 2205: from 48 to 61
 - (B) Polypeptide Sequence
 - Pat. Appln. SEQ ID NO 2206
 - Ceres seq_id 1502616
 - Location of start within SEQ ID NO 2203: at 68 nt.
- - (D) Related Amino Acid Sequences
 - Alignment No. 14441
 - gi No. 3023243
 - % Identity 71.4
 - Alignment Length 14
 - Location of Alignment in SEQ ID NO 2206: from 26 to 39

- (A) Polynucleotide Sequence
 - Pat. Appln. SEQ ID NO 2207
 - Ceres seq_id 1502621
 - (B) Polypeptide Sequence
 - Pat. Appln. SEQ ID NO 2208
 - Ceres seq id 1502622
 - Location of start within SEQ ID NO 2207: at 1 nt.
- - (D) Related Amino Acid Sequences
 - Alignment No. 14442
 - gi No. 330442
 - % Identity 75
 - Alignment Length 12
 - Location of Alignment in SEQ ID NO 2208: from 4 to 15
 - Alignment No. 14443
 - gi No. 3925252
 - % Identity 72.7

- Alignment Length 11
- Location of Alignment in SEQ ID NO 2208: from 35 to 45
- Alignment No. 14444
- qi No. 423830
- % Identity 75
- Alignment Length 12
- Location of Alignment in SEQ ID NO 2208: from 4 to 15
- Alignment No. 14445
- gi No. 4504731
- % Identity 72.7
- Alignment Length 11
- Location of Alignment in SEQ ID NO 2208: from 37 to 47
- Alignment No. 14446
- gi No. 4511969
- % Identity 72.7
- Alignment Length 11
- Location of Alignment in SEQ ID NO 2208: from 37 to 47
- Alignment No. 14447
- gi No. 4838513
- % Identity 71.4
- Alignment Length 14
- Location of Alignment in SEQ ID NO 2208: from 38 to 49
- Alignment No. 14448
- gi No. 4838515
- % Identity 71.4
- Alignment Length 14
- Location of Alignment in SEQ ID NO 2208: from 38 to 49
- Alignment No. 14449
- gi No. 5305335
- % Identity 75
- Alignment Length 12
- Location of Alignment in SEQ ID NO 2208: from 34 to 45
- (B) Polypeptide Sequence
 - Pat. Appln. SEQ ID NO 2209
 - Ceres seq_id 1502623
 - Location of start within SEQ ID NO 2207: at 2 nt.
- (C) Nomination and Annotation of Domains within Predicted Polypeptide(s)
 - (D) Related Amino Acid Sequences
 - Alignment No. 14450
 - gi No. 1722778
 - % Identity 75
 - Alignment Length 12
 - Location of Alignment in SEQ ID NO 2209: from 19 to 30
 - Alignment No. 14451
 - gi No. 5257260
 - % Identity 73.3
 - Alignment Length 15
 - Location of Alignment in SEQ ID NO 2209: from 21 to 35
 - (B) Polypeptide Sequence
 - Pat. Appln. SEQ ID NO 2210

- Ceres seq id 1502624
- Location of start within SEQ ID NO 2207: at 3 nt.
- (C) Nomination and Annotation of Domains within Predicted Polypeptide(s)
 - (D) Related Amino Acid Sequences
 - Alignment No. 14452
 - gi No. 102425
 - % Identity 75
 - Alignment Length 12
 - Location of Alignment in SEQ ID NO 2210: from 28 to 39
 - Alignment No. 14453
 - gi No. 102426
 - % Identity 75
 - Alignment Length 16
 - Location of Alignment in SEQ ID NO 2210: from 28 to 43
 - Alignment No. 14454
 - gi No. 1161370
 - % Identity 81.8
 - Alignment Length 11
 - Location of Alignment in SEQ ID NO 2210: from 26 to 36
 - Alignment No. 14455
 - gi No. 134950
 - % Identity 80
 - Alignment Length 15
 - Location of Alignment in SEQ ID NO 2210: from 23 to 35
 - Alignment No. 14456
 - gi No. 1353462
 - % Identity 72.7
 - Alignment Length 11
 - Location of Alignment in SEQ ID NO 2210: from 26 to 36
 - Alignment No. 14457
 - gi No. 1644455
 - % Identity 71.4
 - Alignment Length 14
 - Location of Alignment in SEQ ID NO 2210: from 28 to 41
 - Alignment No. 14458
 - gi No. 1644457
 - % Identity 71.4
 - Alignment Length 14
 - Location of Alignment in SEQ ID NO 2210: from 28 to 41
 - Alignment No. 14459
 - gi No. 1644459
 - % Identity 71.4
 - Alignment Length 14
 - Location of Alignment in SEQ ID NO 2210: from 28 to 41
 - Alignment No. 14460
 - gi No. 1644461
 - % Identity 71.4
 - Alignment Length 14
 - Location of Alignment in SEQ ID NO 2210: from 28 to 41
 - Alignment No. 14461

- gi No. 2108256
- % Identity 70.6
- Alignment Length 17
- Location of Alignment in SEQ ID NO 2210: from 28 to 43
- Alignment No. 14462
- gi No. 2143272
- % Identity 71.4
- Alignment Length 14
- Location of Alignment in SEQ ID NO 2210: from 28 to 40
- Alignment No. 14463
- gi No. 2257986
- % Identity 75
- Alignment Length 12
- Location of Alignment in SEQ ID NO 2210: from 26 to 37
- Alignment No. 14464
- qi No. 2384847
- % Identity 83.3
- Alignment Length 12
- Location of Alignment in SEQ ID NO 2210: from 22 to 33
- Alignment No. 14465
- gi No. 2384847
- % Identity 75
- Alignment Length 12
- Location of Alignment in SEQ ID NO 2210: from 23 to 34
- Alignment No. 14466
- gi No. 2501953
- % Identity 76.9
- Alignment Length 13
- Location of Alignment in SEQ ID NO 2210: from 28 to 40
- Alignment No. 14467
- gi No. 2950355
- % Identity 73.3
- Alignment Length 15
- Location of Alignment in SEQ ID NO 2210: from 21 to 35
- Alignment No. 14468
- gi No. 310574
- % Identity 90.9
- Alignment Length 11
- Location of Alignment in SEQ ID NO 2210: from 27 to 37
- Alignment No. 14469
- gi No. 310574
- % Identity 90.9
- Alignment Length 11
- Location of Alignment in SEQ ID NO 2210: from 27 to 37
- Alignment No. 14470
- gi No. 3874146
- % Identity 72.7
- Alignment Length 11
- Location of Alignment in SEQ ID NO 2210: from 27 to 37
- Alignment No. 14471
- gi No. 4885040

- % Identity 83.3
- Alignment Length 12
- Location of Alignment in SEQ ID NO 2210: from 28 to 39
- Alignment No. 14472
- gi No. 539033
- % Identity 75
- Alignment Length 16
- Location of Alignment in SEQ ID NO 2210: from 28 to 42
- Alignment No. 14473
- gi No. 5689489
- % Identity 81.8
- Alignment Length 11
- Location of Alignment in SEQ ID NO 2210: from 28 to 38
- Alignment No. 14474
- gi No. 871830
- % Identity 75
- Alignment Length 12
- Location of Alignment in SEQ ID NO 2210: from 28 to 39
- Alignment No. 14475
- gi No. 91094
- % Identity 71.4
- Alignment Length 14
- Location of Alignment in SEQ ID NO 2210: from 21 to 34

- (A) Polynucleotide Sequence
 - Pat. Appln. SEQ ID NO 2211
 - Ceres seq_id 1502635
 - (B) Polypeptide Sequence
 - Pat. Appln. SEQ ID NO 2212
 - Ceres seq id 1502636
 - Location of start within SEQ ID NO 2211: at 88 nt.
- (C) Nomination and Annotation of Domains within Predicted Polypeptide(s)
 - Alignment No. 14476
 - Ribosomal protein S28e
 - Location within SEQ ID NO 2212: from 1 to 65 aa.
 - (D) Related Amino Acid Sequences
 - Alignment No. 14477
 - gi No. 1173237
 - % Identity 92.3
 - Alignment Length 65
 - Location of Alignment in SEQ ID NO 2212: from 1 to 65
 - Alignment No. 14478
 - gi No. 1313916
 - % Identity 71.7
 - Alignment Length 60
 - Location of Alignment in SEQ ID NO 2212: from 6 to 65
 - Alignment No. 14479
 - gi No. 2739219
 - % Identity 92.3
 - Alignment Length 65
 - Location of Alignment in SEQ ID NO 2212: from 1 to 65

- Alignment No. 14480
 gi No. 2995699
 % Identity 71.2
 Alignment Length 66
 Location of Alignment in SEQ ID NO 2212: from 1 to 65
 Alignment No. 14481
 gi No. 3947719
 % Identity 87.7
 Alignment Length 65
- Location of Alignment in SEQ ID NO 2212: from 1 to 65
- Alignment No. 14482
- gi No. 3947725
- % Identity 86.2
- Alignment Length 65
- Location of Alignment in SEQ ID NO 2212: from 1 to 65
- Alignment No. 14483
- gi No. 464714
- % Identity 70.1
- Alignment Length 67
- Location of Alignment in SEQ ID NO 2212: from 1 to 65
- Alignment No. 14484
- gi No. 464715
- % Identity 71.4
- Alignment Length 63
- Location of Alignment in SEQ ID NO 2212: from 3 to 65
- Alignment No. 14485
- gi No. 464720
- % Identity 80
- Alignment Length 65
- Location of Alignment in SEQ ID NO 2212: from 1 to 65
- (B) Polypeptide Sequence
 - Pat. Appln. SEQ ID NO 2213
 - Ceres seq_id 1502637
 - Location of start within SEQ ID NO 2211: at 127 nt.
- - Alignment No. 14486
 - Ribosomal protein S28e
 - Location within SEQ ID NO 2213: from 1 to 52 aa.
 - (D) Related Amino Acid Sequences
 - Alignment No. 14487
 - gi No. 1173237
 - % Identity 92.3
 - Alignment Length 65
 - Location of Alignment in SEQ ID NO 2213: from 1 to 52
 - Alignment No. 14488
 - gi No. 1313916
 - % Identity 71.7
 - Alignment Length 60
 - Location of Alignment in SEQ ID NO 2213: from 1 to 52

- Alignment No. 14489
- gi No. 2739219
- % Identity 92.3
- Alignment Length 65
- Location of Alignment in SEQ ID NO 2213: from 1 to 52
- Alignment No. 14490
- gi No. 2995699
- % Identity 71.2
- Alignment Length 66
- Location of Alignment in SEQ ID NO 2213: from 1 to 52
- Alignment No. 14491
- gi No. 3947719
- % Identity 87.7
- Alignment Length 65
- Location of Alignment in SEQ ID NO 2213: from 1 to 52
- Alignment No. 14492
- gi No. 3947725
- % Identity 86.2
- Alignment Length 65
- Location of Alignment in SEQ ID NO 2213: from 1 to 52
- Alignment No. 14493
- gi No. 464714
- % Identity 70.1
- Alignment Length 67
- Location of Alignment in SEQ ID NO 2213: from 1 to 52
- Alignment No. 14494
- gi No. 464715
- % Identity 71.4
- Alignment Length 63
- Location of Alignment in SEQ ID NO 2213: from 1 to 52
- Alignment No. 14495
- gi No. 464720
- % Identity 80
- Alignment Length 65
- Location of Alignment in SEQ ID NO 2213: from 1 to 52
- (B) Polypeptide Sequence
 - Pat. Appln. SEQ ID NO 2214
 - Ceres seq_id 1502638
 - Location of start within SEQ ID NO 2211: at 209 nt.
- (C) Nomination and Annotation of Domains within Predicted Polypeptide(s)
 - (D) Related Amino Acid Sequences

- (A) Polynucleotide Sequence
 - Pat. Appln. SEQ ID NO 2215
 - Ceres seq_id 1502643
 - (B) Polypeptide Sequence
 - Pat. Appln. SEQ ID NO 2216
 - Ceres seq_id 1502644
 - Location of start within SEQ ID NO 2215: at 2 nt.

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- (C) Nomination and Annotation of Domains within Predicted Polypeptide(s)
 - Alignment No. 14496
 - Zinc finger, C2H2 type
 - Location within SEQ ID NO 2216: from 60 to 82 aa.
 - (D) Related Amino Acid Sequences
 - Alignment No. 14497
 - gi No. 1362015
 - % Identity 74.3
 - Alignment Length 35
 - Location of Alignment in SEQ ID NO 2216: from 57 to 91
 - Alignment No. 14498
 - gi No. 1362020
 - % Identity 75
 - Alignment Length 32
 - Location of Alignment in SEQ ID NO 2216: from 60 to 91
 - Alignment No. 14499
 - gi No. 1362021
 - % Identity 71.4
 - Alignment Length 35
 - Location of Alignment in SEQ ID NO 2216: from 57 to 91
 - Alignment No. 14500
 - gi No. 1871188
 - % Identity 75
 - Alignment Length 32
 - Location of Alignment in SEQ ID NO 2216: from 60 to 91
 - Alignment No. 14501
 - qi No. 790687
 - % Identity 75
 - Alignment Length 32
 - Location of Alignment in SEQ ID NO 2216: from 60 to 91
 - (B) Polypeptide Sequence
 - Pat. Appln. SEQ ID NO 2217
 - Ceres seq_id 1502645
 - Location of start within SEQ ID NO 2215: at 110 nt.
- (C) Nomination and Annotation of Domains within Predicted Polypeptide(s)
 - Alignment No. 14502
 - Zinc finger, C2H2 type
 - Location within SEQ ID NO 2217: from 24 to 46 aa.
 - (D) Related Amino Acid Sequences
 - Alignment No. 14503
 - gi No. 1362015
 - % Identity 74.3
 - Alignment Length 35
 - Location of Alignment in SEQ ID NO 2217: from 21 to 55
 - Alignment No. 14504
 - gi No. 1362020
 - % Identity 75
 - Alignment Length 32
 - Location of Alignment in SEQ ID NO 2217: from 24 to 55

- Alignment No. 14505
- gi No. 1362021
- % Identity 71.4
- Alignment Length 35
- Location of Alignment in SEQ ID NO 2217: from 21 to 55
- Alignment No. 14506
- gi No. 1871188
- % Identity 75
- Alignment Length 32
- Location of Alignment in SEQ ID NO 2217: from 24 to 55
- Alignment No. 14507
- gi No. 790687
- % Identity 75
- Alignment Length 32
- Location of Alignment in SEQ ID NO 2217: from 24 to 55

- (A) Polynucleotide Sequence
 - Pat. Appln. SEQ ID NO 2218
 - Ceres seq_id 1502649
 - (B) Polypeptide Sequence
 - Pat. Appln. SEQ ID NO 2219
 - Ceres seq_id 1502650
 - Location of start within SEQ ID NO 2218: at 2 nt.
- - (D) Related Amino Acid Sequences
 - Alignment No. 14508
 - gi No. 1945621
 - % Identity 100
 - Alignment Length 12
 - Location of Alignment in SEQ ID NO 2219: from 68 to 79
 - Alignment No. 14509
 - gi No. 1945621
 - % Identity 100
 - Alignment Length 12
 - Location of Alignment in SEQ ID NO 2219: from 68 to 79
 - Alignment No. 14510
 - gi No. 1945621
 - % Identity 100
 - Alignment Length 12
 - Location of Alignment in SEQ ID NO 2219: from 68 to 79
 - Alignment No. 14511
 - gi No. 1945621
 - % Identity 100
 - Alignment Length 12
 - Location of Alignment in SEQ ID NO 2219: from 68 to 79
 - Alignment No. 14512
 - gi No. 1945621
 - % Identity 100
 - Alignment Length 12
 - Location of Alignment in SEQ ID NO 2219: from 68 to 79
 - Alignment No. 14513

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- gi No. 2947081
- % Identity 90.9
- Alignment Length 11
- Location of Alignment in SEQ ID NO 2219: from 69 to 79
- Alignment No. 14514
- gi No. 2947081
- % Identity 85.7
- Alignment Length 14
- Location of Alignment in SEQ ID NO 2219: from 68 to 81
- Alignment No. 14515
- gi No. 4097820
- % Identity 83.3
- Alignment Length 12
- Location of Alignment in SEQ ID NO 2219: from 68 to 79
- Alignment No. 14516
- gi No. 4097820
- % Identity 78.6
- Alignment Length 14
- Location of Alignment in SEQ ID NO 2219: from 68 to 81
- Alignment No. 14517
- gi No. 4097820
- % Identity 71.4
- Alignment Length 14
- Location of Alignment in SEQ ID NO 2219: from 67 to 80
- Alignment No. 14518
- gi No. 539415
- % Identity 100
- Alignment Length 11
- Location of Alignment in SEQ ID NO 2219: from 68 to 78
- Alignment No. 14519
- gi No. 539415
- % Identity 91.7
- Alignment Length 12
- Location of Alignment in SEQ ID NO 2219: from 68 to 79
- Alignment No. 14520
- gi No. 539415
- % Identity 91.7
- Alignment Length 12
- Location of Alignment in SEQ ID NO 2219: from 68 to 79
- Alignment No. 14521
- gi No. 539415
- % Identity 83.3
- Alignment Length 12
- Location of Alignment in SEQ ID NO 2219: from 68 to 79
- (B) Polypeptide Sequence
 - Pat. Appln. SEQ ID NO 2220
 - Ceres seq_id 1502651
 - Location of start within SEQ ID NO 2218: at 126 nt.
- (C) Nomination and Annotation of Domains within Predicted Polypeptide(s) $% \left(\frac{1}{2}\right) =\frac{1}{2}\left(\frac{1}{2}\right) +\frac{1}{2}\left(\frac{1}{2}\right) +\frac{$
 - (D) Related Amino Acid Sequences

- (B) Polypeptide Sequence
 - Pat. Appln. SEQ ID NO 2221
 - Ceres seq id 1502652
 - Location of start within SEQ ID NO 2218: at 144 nt.
- - (D) Related Amino Acid Sequences

- (A) Polynucleotide Sequence
 - Pat. Appln. SEQ ID NO 2222
 - Ceres seq_id 1502653
 - (B) Polypeptide Sequence
 - Pat. Appln. SEQ ID NO 2223
 - Ceres seq_id 1502654
 - Location of start within SEQ ID NO 2222: at 1 nt.
- - (D) Related Amino Acid Sequences
 - Alignment No. 14522
 - gi No. 2894228
 - % Identity 73.3
 - Alignment Length 15
 - Location of Alignment in SEQ ID NO 2223: from 9 to 23
 - Alignment No. 14523
 - gi No. 3378540
 - % Identity 71.4
 - Alignment Length 21
 - Location of Alignment in SEQ ID NO 2223: from 4 to 24
 - Alignment No. 14524
 - gi No. 3660471
 - % Identity 87.5
 - Alignment Length 24
 - Location of Alignment in SEQ ID NO 2223: from 1 to 24
 - Alignment No. 14525
 - gi No. 4309723
 - % Identity 79.2
 - Alignment Length 24
 - Location of Alignment in SEQ ID NO 2223: from 1 to 24
 - (B) Polypeptide Sequence
 - Pat. Appln. SEQ ID NO 2224
 - Ceres seq_id 1502655
 - Location of start within SEQ ID NO 2222: at 250 nt.
- (C) Nomination and Annotation of Domains within Predicted Polypeptide(s)
 - (D) Related Amino Acid Sequences
 - Alignment No. 14526
 - gi No. 3660471
 - % Identity 72.2
 - Alignment Length 18
 - Location of Alignment in SEQ ID NO 2224: from 29 to 46
 - Alignment No. 14527

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- gi No. 4309723
- % Identity 72.2
- Alignment Length 18
- Location of Alignment in SEQ ID NO 2224: from 29 to 46
- (B) Polypeptide Sequence
 - Pat. Appln. SEQ ID NO 2225
 - Ceres seq_id 1502656
 - Location of start within SEQ ID NO 2222: at 256 nt.
- - (D) Related Amino Acid Sequences
 - Alignment No. 14528
 - gi No. 3660471
 - % Identity 72.2
 - Alignment Length 18
 - Location of Alignment in SEQ ID NO 2225: from 27 to 44
 - Alignment No. 14529
 - gi No. 4309723
 - % Identity 72.2
 - Alignment Length 18
 - Location of Alignment in SEQ ID NO 2225: from 27 to 44

- (A) Polynucleotide Sequence
 - Pat. Appln. SEQ ID NO 2226
 - Ceres seq_id 1502682
 - (B) Polypeptide Sequence
 - Pat. Appln. SEQ ID NO 2227
 - Ceres seq_id 1502683
 - Location of start within SEQ ID NO 2226: at 2 nt.
- - (D) Related Amino Acid Sequences
 - (B) Polypeptide Sequence
 - Pat. Appln. SEQ ID NO 2228
 - Ceres seq id 1502684
 - Location of start within SEQ ID NO 2226: at 117 nt.
- (C) Nomination and Annotation of Domains within Predicted Polypeptide(s)
 - (D) Related Amino Acid Sequences
 - Alignment No. 14530
 - gi No. 462569
 - % Identity 72.7
 - Alignment Length 11
 - Location of Alignment in SEQ ID NO 2228: from 65 to 75
 - (B) Polypeptide Sequence
 - Pat. Appln. SEQ ID NO 2229
 - Ceres seq_id 1502685
 - Location of start within SEQ ID NO 2226: at 159 nt.
- - (D) Related Amino Acid Sequences
 - Alignment No. 14531

- gi No. 462569
- % Identity 72.7
- Alignment Length 11
- Location of Alignment in SEQ ID NO 2229: from 51 to 61

- (A) Polynucleotide Sequence
 - Pat. Appln. SEQ ID NO 2230
 - Ceres seq_id 1502713
 - (B) Polypeptide Sequence
 - Pat. Appln. SEQ ID NO 2231
 - Ceres seq_id 1502714
 - Location of start within SEQ ID NO 2230: at 3 nt.
- - Alignment No. 14532
 - Asparagine synthase
 - Location within SEQ ID NO 2231: from 1 to 104 aa.
 - (D) Related Amino Acid Sequences
 - Alignment No. 14533
 - gi No. 114260
 - % Identity 70.3
 - Alignment Length 145
 - Location of Alignment in SEQ ID NO 2231: from 1 to 145
 - Alignment No. 14534
 - gi No. 114261
 - % Identity 81.3
 - Alignment Length 123
 - Location of Alignment in SEQ ID NO 2231: from 1 to 123
 - Alignment No. 14535
 - gi No. 1184265
 - % Identity 71.6
 - Alignment Length 134
 - Location of Alignment in SEQ ID NO 2231: from 1 to 134
 - Alignment No. 14536
 - gi No. 1305549
 - % Identity 80.2
 - Alignment Length 121
 - Location of Alignment in SEQ ID NO 2231: from 1 to 121
 - Alignment No. 14537
 - gi No. 1351983
 - % Identity 79.7
 - Alignment Length 123
 - Location of Alignment in SEQ ID NO 2231: from 1 to 123
 - Alignment No. 14538
 - gi No. 1351985
 - % Identity 78
 - Alignment Length 123
 - Location of Alignment in SEQ ID NO 2231: from 1 to 123
 - Alignment No. 14539
 - gi No. 1351987
 - % Identity 80.3
 - Alignment Length 122

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- Location of Alignment in SEQ ID NO 2231: from 1 to 122
- Alignment No. 14540
- gi No. 1351988
- % Identity 73.5
- Alignment Length 132
- Location of Alignment in SEQ ID NO 2231: from 1 to 132
- Alignment No. 14541
- gi No. 1617002
- % Identity 81.1
- Alignment Length 122
- Location of Alignment in SEQ ID NO 2231: from 1 to 122
- Alignment No. 14542
- gi No. 1771880
- % Identity 70.3
- Alignment Length 145
- Location of Alignment in SEQ ID NO 2231: from 1 to 145
- Alignment No. 14543
- gi No. 1778370
- % Identity 78
- Alignment Length 123
- Location of Alignment in SEQ ID NO 2231: from 1 to 123
- Alignment No. 14544
- qi No. 1778372
- % Identity 78.5
- Alignment Length 121
- Location of Alignment in SEQ ID NO 2231: from 1 to 121
- Alignment No. 14545
- gi No. 2429280
- % Identity 83.7
- Alignment Length 123
- Location of Alignment in SEQ ID NO 2231: from 1 to 123
- Alignment No. 14546
- gi No. 2522320
- % Identity 71.6
- Alignment Length 134
- Location of Alignment in SEQ ID NO 2231: from 1 to 134
- Alignment No. 14547
- gi No. 3132675
- % Identity 79.7
- Alignment Length 123
- Location of Alignment in SEQ ID NO 2231: from 1 to 123
- Alignment No. 14548
- gi No. 3182921
- % Identity 86.3
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2231: from 1 to 146
- Alignment No. 14549
- gi No. 3821280
- % Identity 80.5
- Alignment Length 123
- Location of Alignment in SEQ ID NO 2231: from 1 to 123

- Alignment No. 14550
- gi No. 3859534
- % Identity 77.1
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2231: from 1 to 144
- Alignment No. 14551
- gi No. 3859536
- % Identity 76.4
- Alignment Length 144
- Location of Alignment in SEQ ID NO 2231: from 1 to 139
- Alignment No. 14552
- gi No. 3913098
- % Identity 80
- Alignment Length 75
- Location of Alignment in SEQ ID NO 2231: from 1 to 75
- Alignment No. 14553
- gi No. 399064
- % Identity 81.1
- Alignment Length 122
- Location of Alignment in SEQ ID NO 2231: from 1 to 122
- Alignment No. 14554
- qi No. 478402
- % Identity 81.1
- Alignment Length 122
- Location of Alignment in SEQ ID NO 2231: from 1 to 122
- (B) Polypeptide Sequence
 - Pat. Appln. SEQ ID NO 2232
 - Ceres seq id 1502715
 - Location of start within SEQ ID NO 2230: at 132 nt.
- - Alignment No. 14555
 - Asparagine synthase
 - Location within SEQ ID NO 2232: from 1 to 61 aa.
 - (D) Related Amino Acid Sequences
 - Alignment No. 14556
 - gi No. 114260
 - % Identity 70.3
 - Alignment Length 145
 - Location of Alignment in SEQ ID NO 2232: from 1 to 102
 - Alignment No. 14557
 - gi No. 114261
 - % Identity 81.3
 - Alignment Length 123
 - Location of Alignment in SEQ ID NO 2232: from 1 to 80
 - Alignment No. 14558
 - qi No. 1184265
 - % Identity 71.6
 - Alignment Length 134
 - Location of Alignment in SEQ ID NO 2232: from 1 to 91

- Alignment No. 14559
- gi No. 1305549
- % Identity 80.2
- Alignment Length 121
- Location of Alignment in SEQ ID NO 2232: from 1 to 78
- Alignment No. 14560
- gi No. 1351983
- % Identity 79.7
- Alignment Length 123
- Location of Alignment in SEQ ID NO 2232: from 1 to 80
- Alignment No. 14561
- gi No. 1351985
- % Identity 78
- Alignment Length 123
- Location of Alignment in SEQ ID NO 2232: from 1 to 80
- Alignment No. 14562
- gi No. 1351987
- % Identity 80.3
- Alignment Length 122
- Location of Alignment in SEQ ID NO 2232: from 1 to 79
- Alignment No. 14563
- gi No. 1351988
- % Identity 73.5
- Alignment Length 132
- Location of Alignment in SEQ ID NO 2232: from 1 to 89
- Alignment No. 14564
- gi No. 1617002
- % Identity 81.1
- Alignment Length 122
- Location of Alignment in SEQ ID NO 2232: from 1 to 79
- Alignment No. 14565
- gi No. 1771880
- % Identity 70.3
- Alignment Length 145
- Location of Alignment in SEQ ID NO 2232: from 1 to 102
- Alignment No. 14566
- gi No. 1778370
- % Identity 78
- Alignment Length 123
- Location of Alignment in SEQ ID NO 2232: from 1 to 80
- Alignment No. 14567
- gi No. 1778372
- % Identity 78.5
- Alignment Length 121
- Location of Alignment in SEQ ID NO 2232: from 1 to 78
- Alignment No. 14568
- gi No. 2429280
- % Identity 83.7
- Alignment Length 123
- Location of Alignment in SEQ ID NO 2232: from 1 to 80
- Alignment No. 14569

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- gi No. 2522320
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- % Identity 71.6
- Alignment Length 134
- Location of Alignment in SEQ ID NO 2232: from 1 to 91
- Alignment No. 14570
- gi No. 3132675
- % Identity 79.7
- Alignment Length 123
- Location of Alignment in SEQ ID NO 2232: from 1 to 80
- Alignment No. 14571
- gi No. 3182921
- % Identity 86.3
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2232: from 1 to 103
- Alignment No. 14572
- gi No. 3821280
- % Identity 80.5
- Alignment Length 123
- Location of Alignment in SEQ ID NO 2232: from 1 to 80
- Alignment No. 14573
- gi No. 3859534
- % Identity 77.1
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2232: from 1 to 101
- Alignment No. 14574
- gi No. 3859536
- % Identity 76.4
- Alignment Length 144
- Location of Alignment in SEQ ID NO 2232: from 1 to 96
- Alignment No. 14575
- gi No. 3913098
- % Identity 80
- Alignment Length 75
- Location of Alignment in SEQ ID NO 2232: from 1 to 32
- Alignment No. 14576
- gi No. 399064
- % Identity 81.1
- Alignment Length 122
- Location of Alignment in SEQ ID NO 2232: from 1 to 79
- Alignment No. 14577
- gi No. 478402
- % Identity 81.1
- Alignment Length 122
- Location of Alignment in SEQ ID NO 2232: from 1 to 79
- (B) Polypeptide Sequence
 - Pat. Appln. SEQ ID NO 2233
 - Ceres seq_id 1502716
 - Location of start within SEQ ID NO 2230: at 135 nt.
- (C) Nomination and Annotation of Domains within Predicted Polypeptide(s) $\label{eq:condition}$
 - Alignment No. 14578

- Asparagine synthase
- Location within SEQ ID NO 2233: from 1 to 60 aa.
- (D) Related Amino Acid Sequences
 - Alignment No. 14579
 - gi No. 114260
 - % Identity 70.3
 - Alignment Length 145
 - Location of Alignment in SEQ ID NO 2233: from 1 to 101
 - Alignment No. 14580
 - gi No. 114261
 - % Identity 81.3
 - Alignment Length 123
 - Location of Alignment in SEQ ID NO 2233: from 1 to 79
 - Alignment No. 14581
 - gi No. 1184265
 - % Identity 71.6
 - Alignment Length 134
 - Location of Alignment in SEQ ID NO 2233: from 1 to 90
 - Alignment No. 14582
 - gi No. 1305549
 - % Identity 80.2
 - Alignment Length 121
 - Location of Alignment in SEQ ID NO 2233: from 1 to 77
 - Alignment No. 14583
 - gi No. 1351983
 - % Identity 79.7
 - Alignment Length 123
 - Location of Alignment in SEQ ID NO 2233: from 1 to 79
 - Alignment No. 14584
 - gi No. 1351985
 - % Identity 78
 - Alignment Length 123
 - Location of Alignment in SEQ ID NO 2233: from 1 to 79
 - Alignment No. 14585
 - gi No. 1351987
 - % Identity 80.3
 - Alignment Length 122
 - Location of Alignment in SEQ ID NO 2233: from 1 to 78
 - Alignment No. 14586
 - gi No. 1351988
 - % Identity 73.5
 - Alignment Length 132
 - Location of Alignment in SEQ ID NO 2233: from 1 to 88
 - Alignment No. 14587
 - gi No. 1617002
 - % Identity 81.1
 - Alignment Length 122
 - Location of Alignment in SEQ ID NO 2233: from 1 to 78
 - Alignment No. 14588
 - gi No. 1771880
 - % Identity 70.3

- % Identity 80 - Alignment Length 75

- Alignment Length 145 - Location of Alignment in SEQ ID NO 2233: from 1 to 101 - Alignment No. 14589 - gi No. 1778370 - % Identity 78 - Alignment Length 123 - Location of Alignment in SEQ ID NO 2233: from 1 to 79 - Alignment No. 14590 - gi No. 1778372 - % Identity 78.5 - Alignment Length 121 - Location of Alignment in SEQ ID NO 2233: from 1 to 77 - Alignment No. 14591 - gi No. 2429280 - % Identity 83.7 - Alignment Length 123 - Location of Alignment in SEQ ID NO 2233: from 1 to 79 - Alignment No. 14592 - qi No. 2522320 - % Identity 71.6 - Alignment Length 134 - Location of Alignment in SEQ ID NO 2233: from 1 to 90 - Alignment No. 14593 - gi No. 3132675 - % Identity 79.7 - Alignment Length 123 - Location of Alignment in SEQ ID NO 2233: from 1 to 79 - Alignment No. 14594 - gi No. 3182921 - % Identity 86.3 - Alignment Length 146 - Location of Alignment in SEQ ID NO 2233: from 1 to 102 - Alignment No. 14595 - gi No. 3821280 - % Identity 80.5 - Alignment Length 123 - Location of Alignment in SEQ ID NO 2233: from 1 to 79 - Alignment No. 14596 - gi No. 3859534 - % Identity 77.1 - Alignment Length 146 - Location of Alignment in SEQ ID NO 2233: from 1 to 100 - Alignment No. 14597 - gi No. 3859536 - % Identity 76.4 - Alignment Length 144 - Location of Alignment in SEQ ID NO 2233: from 1 to 95 - Alignment No. 14598 - gi No. 3913098

- Location of Alignment in SEQ ID NO 2233: from 1 to 31
- Alignment No. 14599
- gi No. 399064
- % Identity 81.1
- Alignment Length 122
- Location of Alignment in SEQ ID NO 2233: from 1 to 78
- Alignment No. 14600
- gi No. 478402
- % Identity 81.1
- Alignment Length 122
- Location of Alignment in SEQ ID NO 2233: from 1 to 78

- (A) Polynucleotide Sequence
 - Pat. Appln. SEQ ID NO 2234
 - Ceres seg id 1502717
 - (B) Polypeptide Sequence
 - Pat. Appln. SEQ ID NO 2235
 - Ceres seq_id 1502718
 - Location of start within SEQ ID NO 2234: at 136 nt.
- (C) Nomination and Annotation of Domains within Predicted Polypeptide(s) $\label{eq:continuous} % \begin{array}{c} \text{Polypertide}(s) \\ \text$
 - (D) Related Amino Acid Sequences
 - Alignment No. 14601
 - gi No. 1778093
 - % Identity 73.5
 - Alignment Length 34
 - Location of Alignment in SEQ ID NO 2235: from 1 to 19
 - Alignment No. 14602
 - gi No. 1778095
 - % Identity 73.5
 - Alignment Length 34
 - Location of Alignment in SEQ ID NO 2235: from 1 to 19
 - Alignment No. 14603
 - gi No. 4678208
 - % Identity 71
 - Alignment Length 31
 - Location of Alignment in SEQ ID NO 2235: from 1 to 19
 - (B) Polypeptide Sequence
 - Pat. Appln. SEQ ID NO 2236
 - Ceres seq_id 1502719
 - Location of start within SEQ ID NO 2234: at 172 nt.
- - (D) Related Amino Acid Sequences
 - (B) Polypeptide Sequence
 - Pat. Appln. SEQ ID NO 2237
 - Ceres seq_id 1502720
 - Location of start within SEQ ID NO 2234: at 194 nt.
- (C) Nomination and Annotation of Domains within Predicted Polypeptide(s)
 - (D) Related Amino Acid Sequences

- (A) Polynucleotide Sequence
 - Pat. Appln. SEQ ID NO 2238
 - Ceres seq id 1502721
 - (B) Polypeptide Sequence
 - Pat. Appln. SEQ ID NO 2239
 - Ceres seq id 1502722
 - Location of start within SEQ ID NO 2238: at 1 nt.
- - (D) Related Amino Acid Sequences
 - Alignment No. 14604
 - gi No. 1705677
 - % Identity 76.1
 - Alignment Length 109
 - Location of Alignment in SEQ ID NO 2239: from 1 to 108
 - Alignment No. 14605
 - gi No. 1705678
 - % Identity 75.9
 - Alignment Length 111
 - Location of Alignment in SEQ ID NO 2239: from 1 to 108
 - Alignment No. 14606
 - gi No. 2492504
 - % Identity 77.8
 - Alignment Length 108
 - Location of Alignment in SEQ ID NO 2239: from 1 to 108
 - (B) Polypeptide Sequence
 - Pat. Appln. SEQ ID NO 2240
 - Ceres seq id 1502723
 - Location of start within SEQ ID NO 2238: at 70 nt.
- (C) Nomination and Annotation of Domains within Predicted Polypeptide(s) $% \left(\frac{1}{2}\right) =\frac{1}{2}\left(\frac{1}{2}\right) +\frac{1}{2}\left(\frac{1}{2}\right) +\frac{$
 - (D) Related Amino Acid Sequences
 - Alignment No. 14607
 - gi No. 1705677
 - % Identity 76.1
 - Alignment Length 109
 - Location of Alignment in SEQ ID NO 2240: from 1 to 85
 - Alignment No. 14608
 - gi No. 1705678
 - % Identity 75.9
 - Alignment Length 111
 - Location of Alignment in SEQ ID NO 2240: from 1 to 85
 - Alignment No. 14609
 - gi No. 2492504
 - % Identity 77.8
 - Alignment Length 108
 - Location of Alignment in SEQ ID NO 2240: from 1 to 85
 - (B) Polypeptide Sequence
 - Pat. Appln. SEQ ID NO 2241
 - Ceres seq id 1502724
 - Location of start within SEQ ID NO 2238: at 137 nt.

- - (D) Related Amino Acid Sequences

- (A) Polynucleotide Sequence
 - Pat. Appln. SEQ ID NO 2242
 - Ceres seq id 1502726
 - (B) Polypeptide Sequence
 - Pat. Appln. SEQ ID NO 2243
 - Ceres seq id 1502727
 - Location of start within SEQ ID NO 2242: at 2 nt.
- - (D) Related Amino Acid Sequences
 - (B) Polypeptide Sequence
 - Pat. Appln. SEQ ID NO 2244
 - Ceres seq_id 1502728
 - Location of start within SEQ ID NO 2242: at 3 nt.
- - Alignment No. 14610
 - 7 transmembrane receptor (rhodopsin family)
 - Location within SEQ ID NO 2244: from 21 to 78 aa.
 - (D) Related Amino Acid Sequences
 - (B) Polypeptide Sequence
 - Pat. Appln. SEQ ID NO 2245
 - Ceres seq_id 1502729
 - Location of start within SEQ ID NO 2242: at 20 nt.
- (C) Nomination and Annotation of Domains within Predicted Polypeptide(s)
 - (D) Related Amino Acid Sequences

- (A) Polynucleotide Sequence
 - Pat. Appln. SEQ ID NO 2246
 - Ceres seq_id 1502730
 - (B) Polypeptide Sequence
 - Pat. Appln. SEQ ID NO 2247
 - Ceres seq_id 1502731
 - Location of start within SEQ ID NO 2246: at 114 nt.
- - (D) Related Amino Acid Sequences
 - Alignment No. 14611
 - gi No. 2500047
 - % Identity 87.5
 - Alignment Length 40
 - Location of Alignment in SEQ ID NO 2247: from 15 to 54
 - Alignment No. 14612
 - gi No. 3510259
 - % Identity 73.2

- Alignment Length 56
- Location of Alignment in SEQ ID NO 2247: from 1 to 54
- Alignment No. 14613
- gi No. 4033417
- % Identity 77.2
- Alignment Length 57
- Location of Alignment in SEQ ID NO 2247: from 1 to 54
- Alignment No. 14614
- gi No. 4033424
- % Identity 100
- Alignment Length 54
- Location of Alignment in SEQ ID NO 2247: from 1 to 54

- (A) Polynucleotide Sequence
 - Pat. Appln. SEQ ID NO 2248
 - Ceres seq_id 1502755
 - (B) Polypeptide Sequence
 - Pat. Appln. SEQ ID NO 2249
 - Ceres seq_id 1502756
 - Location of start within SEQ ID NO 2248: at 1 nt.
- (C) Nomination and Annotation of Domains within Predicted Polypeptide(s) $\label{eq:continuous} % \begin{array}{c} (C) & (C)$
 - (D) Related Amino Acid Sequences
 - (B) Polypeptide Sequence
 - Pat. Appln. SEQ ID NO 2250
 - Ceres seq_id 1502757
 - Location of start within SEQ ID NO 2248: at 2 nt.
- - (D) Related Amino Acid Sequences
 - Alignment No. 14615
 - gi No. 2129800
 - % Identity 71.4
 - Alignment Length 21
 - Location of Alignment in SEQ ID NO 2250: from 68 to 87
 - Alignment No. 14616
 - gi No. 2129804
 - % Identity 71.4
 - Alignment Length 21
 - Location of Alignment in SEQ ID NO 2250: from 68 to 87
 - Alignment No. 14617
 - gi No. 2129805
 - % Identity 71.4
 - Alignment Length 21
 - Location of Alignment in SEQ ID NO 2250: from 68 to 87
 - Alignment No. 14618
 - gi No. 2317758
 - % Identity 76.2
 - Alignment Length 21
 - Location of Alignment in SEQ ID NO 2250: from 68 to 87
 - Alignment No. 14619

- gi No. 2317758
- % Identity 72
- Alignment Length 25
- Location of Alignment in SEQ ID NO 2250: from 65 to 87
- Alignment No. 14620
- gi No. 5391446
- % Identity 76.2
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2250: from 68 to 87
- (B) Polypeptide Sequence
 - Pat. Appln. SEQ ID NO 2251
 - Ceres seq_id 1502758
 - Location of start within SEQ ID NO 2248: at 3 nt.
- - (D) Related Amino Acid Sequences

- (A) Polynucleotide Sequence
 - Pat. Appln. SEQ ID NO 2252
 - Ceres seq_id 1502759
 - (B) Polypeptide Sequence
 - Pat. Appln. SEQ ID NO 2253
 - Ceres seq_id 1502760
 - Location of start within SEQ ID NO 2252: at 2 nt.
- - (D) Related Amino Acid Sequences
 - (B) Polypeptide Sequence
 - Pat. Appln. SEQ ID NO 2254
 - Ceres seq_id 1502761
 - Location of start within SEQ ID NO 2252: at 3 nt.
- - (D) Related Amino Acid Sequences
 - Alignment No. 14621
 - gi No. 2781345
 - % Identity 79.3
 - Alignment Length 58
 - Location of Alignment in SEQ ID NO 2254: from 1 to 58
 - Alignment No. 14622
 - gi No. 3157933
 - % Identity 76.1
 - Alignment Length 71
 - Location of Alignment in SEQ ID NO 2254: from 1 to 71
 - (B) Polypeptide Sequence
 - Pat. Appln. SEQ ID NO 2255
 - Ceres seq_id 1502762
 - Location of start within SEQ ID NO 2252: at 320 nt.
- - (D) Related Amino Acid Sequences

- (A) Polynucleotide Sequence
 - Pat. Appln. SEQ ID NO 2256
 - Ceres seq id 1502763
 - (B) Polypeptide Sequence
 - Pat. Appln. SEQ ID NO 2257
 - Ceres seq id 1502764
 - Location of start within SEQ ID NO 2256: at 1 nt.
- - (D) Related Amino Acid Sequences
 - Alignment No. 14623
 - gi No. 4512216
 - % Identity 80.5
 - Alignment Length 41
 - Location of Alignment in SEQ ID NO 2257: from 114 to 154
 - Alignment No. 14624
 - gi No. 5689236
 - % Identity 75.6
 - Alignment Length 41
 - Location of Alignment in SEQ ID NO 2257: from 114 to 154
 - (B) Polypeptide Sequence
 - Pat. Appln. SEQ ID NO 2258
 - Ceres seq_id 1502765
 - Location of start within SEQ ID NO 2256: at 2 nt.
- - (D) Related Amino Acid Sequences
 - (B) Polypeptide Sequence
 - Pat. Appln. SEQ ID NO 2259
 - Ceres seq_id 1502766
 - Location of start within SEQ ID NO 2256: at 8 nt.
- - (D) Related Amino Acid Sequences

- (A) Polynucleotide Sequence
 - Pat. Appln. SEQ ID NO 2260
 - Ceres seq_id 1502767
 - (B) Polypeptide Sequence
 - Pat. Appln. SEQ ID NO 2261
 - Ceres seq_id 1502768
 - Location of start within SEQ ID NO 2260: at 3 nt.
- (C) Nomination and Annotation of Domains within Predicted Polypeptide(s)
 - (D) Related Amino Acid Sequences
 - (B) Polypeptide Sequence
 - Pat. Appln. SEQ ID NO 2262
 - Ceres seq id 1502769
 - Location of start within SEQ ID NO 2260: at 135 nt.

- - (D) Related Amino Acid Sequences
 - (B) Polypeptide Sequence
 - Pat. Appln. SEQ ID NO 2263
 - Ceres seq id 1502770
 - Location of start within SEQ ID NO 2260: at 250 nt.
- - (D) Related Amino Acid Sequences
 - Alignment No. 14625
 - gi No. 5262791
 - % Identity 78.6
 - Alignment Length 14
 - Location of Alignment in SEQ ID NO 2263: from 57 to 69

- (A) Polynucleotide Sequence
 - Pat. Appln. SEQ ID NO 2264
 - Ceres seq id 1502771
 - (B) Polypeptide Sequence
 - Pat. Appln. SEQ ID NO 2265
 - Ceres seq_id 1502772
 - Location of start within SEQ ID NO 2264: at 2 nt.
- - (D) Related Amino Acid Sequences
 - Alignment No. 14626
 - gi No. 2149640
 - % Identity 81.2
 - Alignment Length 101
 - Location of Alignment in SEQ ID NO 2265: from 1 to 99
 - Alignment No. 14627
 - gi No. 2959781
 - % Identity 70.7
 - Alignment Length 101
 - Location of Alignment in SEQ ID NO 2265: from 1 to 99
 - Alignment No. 14628
 - gi No. 5107374
 - % Identity 70.7
 - Alignment Length 101
 - Location of Alignment in SEQ ID NO 2265: from 1 to 99
 - (B) Polypeptide Sequence
 - Pat. Appln. SEQ ID NO 2266
 - Ceres seq_id 1502773
 - Location of start within SEQ ID NO 2264: at 146 nt.
- (C) Nomination and Annotation of Domains within Predicted Polypeptide(s)
 - (D) Related Amino Acid Sequences
 - Alignment No. 14629
 - gi No. 2149640
 - % Identity 81.2
 - Alignment Length 101
 - Location of Alignment in SEQ ID NO 2266: from 1 to 51

- Alignment No. 14630
- gi No. 2959781
- % Identity 70.7
- Alignment Length 101
- Location of Alignment in SEQ ID NO 2266: from 1 to 51
- Alignment No. 14631
- gi No. 5107374
- % Identity 70.7
- Alignment Length 101
- Location of Alignment in SEQ ID NO 2266: from 1 to 51

- (A) Polynucleotide Sequence
 - Pat. Appln. SEQ ID NO 2267
 - Ceres seq_id 1502781
 - (B) Polypeptide Sequence
 - Pat. Appln. SEQ ID NO 2268
 - Ceres seq_id 1502782
 - Location of start within SEQ ID NO 2267: at 2 nt.
- - (D) Related Amino Acid Sequences
 - (B) Polypeptide Sequence
 - Pat. Appln. SEQ ID NO 2269
 - Ceres seq id 1502783
 - Location of start within SEQ ID NO 2267: at 3 nt.
- - (D) Related Amino Acid Sequences
 - Alignment No. 14632
 - gi No. 3264598
 - % Identity 76
 - Alignment Length 25
 - Location of Alignment in SEQ ID NO 2269: from 19 to 39

- (A) Polynucleotide Sequence
 - Pat. Appln. SEQ ID NO 2270
 - Ceres seq_id 1502784
 - (B) Polypeptide Sequence
 - Pat. Appln. SEQ ID NO 2271
 - Ceres seq_id 1502785
 - Location of start within SEQ ID NO 2270: at 1 nt.
- (C) Nomination and Annotation of Domains within Predicted Polypeptide(s) $\label{eq:condition} % \begin{array}{c} (C) & (C)$
 - (D) Related Amino Acid Sequences
 - (B) Polypeptide Sequence
 - Pat. Appln. SEQ ID NO 2272
 - Ceres seq_id 1502786
 - Location of start within SEQ ID NO 2270: at 2 nt.
- (C) Nomination and Annotation of Domains within Predicted Polypeptide(s)
 - (D) Related Amino Acid Sequences

- (B) Polypeptide Sequence
 - Pat. Appln. SEQ ID NO 2273
 - Ceres seq id 1502787
 - Location of start within SEQ ID NO 2270: at 3 nt.
- - (D) Related Amino Acid Sequences
 - Alignment No. 14633
 - gi No. 102706
 - % Identity 77.8
 - Alignment Length 18
 - Location of Alignment in SEQ ID NO 2273: from 4 to 19
 - Alignment No. 14634
 - gi No. 1042189
 - % Identity 80
 - Alignment Length 15
 - Location of Alignment in SEQ ID NO 2273: from 5 to 19
 - Alignment No. 14635
 - gi No. 1168711
 - % Identity 78.6
 - Alignment Length 14
 - Location of Alignment in SEQ ID NO 2273: from 5 to 18
 - Alignment No. 14636
 - gi No. 131044
 - % Identity 77.8
 - Alignment Length 18
 - Location of Alignment in SEQ ID NO 2273: from 4 to 19
 - Alignment No. 14637
 - gi No. 1362586
 - % Identity 77.8
 - Alignment Length 18
 - Location of Alignment in SEQ ID NO 2273: from 4 to 19
 - Alignment No. 14638
 - gi No. 1362587
 - % Identity 80
 - Alignment Length 15
 - Location of Alignment in SEQ ID NO 2273: from 5 to 19
 - Alignment No. 14639
 - gi No. 1362587
 - % Identity 80
 - Alignment Length 15
 - Location of Alignment in SEQ ID NO 2273: from 5 to 19

- (A) Polynucleotide Sequence
 - Pat. Appln. SEQ ID NO 2274
 - Ceres seq_id 1502805
 - (B) Polypeptide Sequence
 - Pat. Appln. SEQ ID NO 2275
 - Ceres seq id 1502806
 - Location of start within SEQ ID NO 2274: at 123 nt.

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- (C) Nomination and Annotation of Domains within Predicted Polypeptide(s)
 - Alignment No. 14640
 - Macrophage migration inhibitory factor (MIF)
 - Location within SEQ ID NO 2275: from 2 to 104 aa.
 - (D) Related Amino Acid Sequences
 - (B) Polypeptide Sequence
 - Pat. Appln. SEQ ID NO 2276
 - Ceres seq id 1502807
 - Location of start within SEQ ID NO 2274: at 240 nt.
- - Alignment No. 14641
 - Macrophage migration inhibitory factor (MIF)
 - Location within SEQ ID NO 2276: from 1 to 65 aa.
 - (D) Related Amino Acid Sequences
 - (B) Polypeptide Sequence
 - Pat. Appln. SEQ ID NO 2277
 - Ceres seq id 1502808
 - Location of start within SEQ ID NO 2274: at 267 nt.
- - Alignment No. 14642
 - Macrophage migration inhibitory factor (MIF)
 - Location within SEQ ID NO 2277: from 1 to 56 aa.
 - (D) Related Amino Acid Sequences

- (A) Polynucleotide Sequence
 - Pat. Appln. SEQ ID NO 2278
 - Ceres seq_id 1502809
 - (B) Polypeptide Sequence
 - Pat. Appln. SEQ ID NO 2279
 - Ceres seq_id 1502810
 - Location of start within SEQ ID NO 2278: at 1 nt.
- (C) Nomination and Annotation of Domains within Predicted Polypeptide(s) $% \left(\frac{1}{2}\right) =\frac{1}{2}\left(\frac{1}{2}\right) +\frac{1}{2}\left(\frac{1}{2}\right) +\frac{$
 - (D) Related Amino Acid Sequences
 - (B) Polypeptide Sequence
 - Pat. Appln. SEQ ID NO 2280
 - Ceres seq id 1502811
 - Location of start within SEQ ID NO 2278: at 3 nt.
- (C) Nomination and Annotation of Domains within Predicted Polypeptide(s)
 - (D) Related Amino Acid Sequences
 - Alignment No. 14643
 - gi No. 4115377
 - % Identity 82.8
 - Alignment Length 58
 - Location of Alignment in SEQ ID NO 2280: from 58 to 115

- (A) Polynucleotide Sequence
 - Pat. Appln. SEQ ID NO 2281
 - Ceres seq_id 1502820
 - (B) Polypeptide Sequence
 - Pat. Appln. SEQ ID NO 2282
 - Ceres seq_id 1502821
 - Location of start within SEQ ID NO 2281: at 3 nt.
- - (D) Related Amino Acid Sequences
 - (B) Polypeptide Sequence
 - Pat. Appln. SEQ ID NO 2283
 - Ceres seq_id 1502822
 - Location of start within SEQ ID NO 2281: at 101 nt.
- (C) Nomination and Annotation of Domains within Predicted Polypeptide(s)
 - Alignment No. 14644
 - Ribosomal protein S11
 - Location within SEQ ID NO 2283: from 28 to 105 aa.
 - (D) Related Amino Acid Sequences
 - Alignment No. 14645
 - gi No. 1173200
 - % Identity 82.1
 - Alignment Length 39
 - Location of Alignment in SEQ ID NO 2283: from 67 to 105
 - Alignment No. 14646
 - gi No. 1173201
 - % Identity 82.2
 - Alignment Length 101
 - Location of Alignment in SEQ ID NO 2283: from 5 to 105
 - Alignment No. 14647
 - gi No. 131772
 - % Identity 92.4
 - Alignment Length 105
 - Location of Alignment in SEQ ID NO 2283: from 1 to 105
 - Alignment No. 14648
 - gi No. 131773
 - % Identity 89.3
 - Alignment Length 103
 - Location of Alignment in SEQ ID NO 2283: from 3 to 105
 - Alignment No. 14649
 - gi No. 133771
 - % Identity 74.5
 - Alignment Length 106
 - Location of Alignment in SEQ ID NO 2283: from 1 to 105
 - Alignment No. 14650
 - gi No. 133777
 - % Identity 77.6
 - Alignment Length 85
 - Location of Alignment in SEQ ID NO 2283: from 21 to 105

- Alignment No. 14651 - gi No. 133782 - % Identity 72.9 - Alignment Length 107 - Location of Alignment in SEQ ID NO 2283: from 1 to 105 - Alignment No. 14652 - gi No. 133785 - % Identity 78.3 - Alignment Length 106 - Location of Alignment in SEQ ID NO 2283: from 1 to 105 - Alignment No. 14653 - gi No. 1346941 - % Identity 74.1 - Alignment Length 85 - Location of Alignment in SEQ ID NO 2283: from 21 to 105 - Alignment No. 14654 - gi No. 1350935 - % Identity 74.8 - Alignment Length 107 - Location of Alignment in SEQ ID NO 2283: from 1 to 105 - Alignment No. 14655 - gi No. 2350992 - % Identity 77 - Alignment Length 74 - Location of Alignment in SEQ ID NO 2283: from 27 to 100 - Alignment No. 14656 - gi No. 2414647 - % Identity 80.5 - Alignment Length 87 - Location of Alignment in SEQ ID NO 2283: from 16 to 102 - Alignment No. 14657 - gi No. 2500442 - % Identity 70.5 - Alignment Length 78 - Location of Alignment in SEQ ID NO 2283: from 4 to 80 - Alignment No. 14658 - gi No. 2500443 - % Identity 71.4 - Alignment Length 21 - Location of Alignment in SEQ ID NO 2283: from 85 to 105 - Alignment No. 14659 - gi No. 3097244 - % Identity 80.2 - Alignment Length 106 - Location of Alignment in SEQ ID NO 2283: from 1 to 105
- Alignment No. 14660
- gi No. 3122785
- % Identity 84.8
- Alignment Length 105
- Location of Alignment in SEQ ID NO 2283: from 1 to 105
- Alignment No. 14661

- gi No. 4574240
- % Identity 77.6
- Alignment Length 85
- Location of Alignment in SEQ ID NO 2283: from 21 to 105
- Alignment No. 14662
- gi No. 4588920
- % Identity 74.5
- Alignment Length 106
- Location of Alignment in SEQ ID NO 2283: from 1 to 105
- Alignment No. 14663
- gi No. 4678226
- % Identity 84.8
- Alignment Length 105
- Location of Alignment in SEQ ID NO 2283: from 1 to 105
- Alignment No. 14664
- gi No. 4886269
- % Identity 85.7
- Alignment Length 105
- Location of Alignment in SEQ ID NO 2283: from 1 to 105
- Alignment No. 14665
- gi No. 5032051
- % Identity 79.2
- Alignment Length 106
- Location of Alignment in SEQ ID NO 2283: from 1 to 105
- Alignment No. 14666
- gi No. 5441523
- % Identity 88.2
- Alignment Length 34
- Location of Alignment in SEQ ID NO 2283: from 72 to 105
- Alignment No. 14667
- gi No. 547604
- % Identity 75.3
- Alignment Length 85
- Location of Alignment in SEQ ID NO 2283: from 21 to 105
- Alignment No. 14668
- gi No. 70946
- % Identity 74.1
- Alignment Length 85
- Location of Alignment in SEQ ID NO 2283: from 21 to 105
- Alignment No. 14669
- gi No. 730453
- % Identity 75.3
- Alignment Length 85
- Location of Alignment in SEQ ID NO 2283: from 21 to 105
- Alignment No. 14670
- gi No. 730633
- % Identity 76.4
- Alignment Length 106
- Location of Alignment in SEQ ID NO 2283: from 1 to 105
- Alignment No. 14671
- gi No. 83794

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- % Identity 74.3
- Alignment Length 105
- Location of Alignment in SEQ ID NO 2283: from 1 to 105

Maximum Length Sequence corresponding to clone ID 312649

- (A) Polynucleotide Sequence
 - Pat. Appln. SEQ ID NO 2284
 - Ceres seq_id 1502834
 - (B) Polypeptide Sequence
 - Pat. Appln. SEQ ID NO 2285
 - Ceres seq_id 1502835
 - Location of start within SEQ ID NO 2284: at 3 nt.
- (C) Nomination and Annotation of Domains within Predicted Polypeptide(s)
 - Alignment No. 14672
 - Forkhead-associated (FHA) domain
 - Location within SEQ ID NO 2285: from 92 to 145 aa.
 - (D) Related Amino Acid Sequences
 - (B) Polypeptide Sequence
 - Pat. Appln. SEQ ID NO 2286
 - Ceres seq id 1502836
 - Location of start within SEQ ID NO 2284: at 57 nt.
- - Alignment No. 14673
 - Forkhead-associated (FHA) domain
 - Location within SEQ ID NO 2286: from 74 to 127 aa.
 - (D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 312672

- (A) Polynucleotide Sequence
 - Pat. Appln. SEQ ID NO 2287
 - Ceres seq_id 1502844
 - (B) Polypeptide Sequence
 - Pat. Appln. SEQ ID NO 2288
 - Ceres seq_id 1502845
 - Location of start within SEQ ID NO 2287: at 1 nt.
- - Alignment No. 14674
 - DnaJ domain
 - Location within SEQ ID NO 2288: from 1 to 29 aa.
 - (D) Related Amino Acid Sequences

- (A) Polynucleotide Sequence
 - Pat. Appln. SEQ ID NO 2289
 - Ceres seq_id 1502850
 - (B) Polypeptide Sequence
 - Pat. Appln. SEQ ID NO 2290
 - Ceres seq id 1502851
 - Location of start within SEQ ID NO 2289: at 2 nt.

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- (C) Nomination and Annotation of Domains within Predicted Polypeptide(s)
 - (D) Related Amino Acid Sequences
 - (B) Polypeptide Sequence
 - Pat. Appln. SEQ ID NO 2291
 - Ceres seq id 1502852
 - Location of start within SEQ ID NO 2289: at 144 nt.
- (C) Nomination and Annotation of Domains within Predicted Polypeptide(s)
 - (D) Related Amino Acid Sequences
 - (B) Polypeptide Sequence
 - Pat. Appln. SEQ ID NO 2292
 - Ceres seq id 1502853
 - Location of start within SEQ ID NO 2289: at 217 nt.
- (C) Nomination and Annotation of Domains within Predicted Polypeptide(s)
 - (D) Related Amino Acid Sequences
 - Alignment No. 14675
 - gi No. 4220472
 - % Identity 76.3
 - Alignment Length 38
 - Location of Alignment in SEQ ID NO 2292: from 1 to 19

- (A) Polynucleotide Sequence
 - Pat. Appln. SEQ ID NO 2293
 - Ceres seq id 1502860
 - (B) Polypeptide Sequence
 - Pat. Appln. SEQ ID NO 2294
 - Ceres seq_id 1502861
 - Location of start within SEQ ID NO 2293: at 2 nt.
- (C) Nomination and Annotation of Domains within Predicted Polypeptide(s)
 - (D) Related Amino Acid Sequences
 - (B) Polypeptide Sequence
 - Pat. Appln. SEQ ID NO 2295
 - Ceres seq id 1502862
 - Location of start within SEO ID NO 2293: at 3 nt.
- (C) Nomination and Annotation of Domains within Predicted Polypeptide(s)
 - Alignment No. 14676
 - Plant lipid transfer protein family
 - Location within SEQ ID NO 2295: from 75 to 153 aa.
 - (D) Related Amino Acid Sequences
 - Alignment No. 14677
 - gi No. 1084462
 - % Identity 70
 - Alignment Length 81
 - Location of Alignment in SEQ ID NO 2295: from 75 to 152
 - Alignment No. 14678
 - gi No. 2226329
 - % Identity 93.8

- Alignment Length 80
- Location of Alignment in SEQ ID NO 2295: from 75 to 154
- Alignment No. 14679
- gi No. 399204
- % Identity 92.5
- Alignment Length 80
- Location of Alignment in SEQ ID NO 2295: from 75 to 154

- (A) Polynucleotide Sequence
 - Pat. Appln. SEQ ID NO 2296
 - Ceres seq id 1502896
 - (B) Polypeptide Sequence
 - Pat. Appln. SEQ ID NO 2297
 - Ceres seq id 1502897
 - Location of start within SEQ ID NO 2296: at 1 nt.
- (C) Nomination and Annotation of Domains within Predicted Polypeptide(s) $\label{eq:continuous} % \begin{array}{c} (C) & (C)$
 - Alignment No. 14680
 - Eukaryotic protein kinase domain
 - Location within SEQ ID NO 2297: from 1 to 101 aa.
 - (D) Related Amino Acid Sequences
 - Alignment No. 14681
 - gi No. 100610
 - % Identity 80.2
 - Alignment Length 111
 - Location of Alignment in SEQ ID NO 2297: from 1 to 110
 - Alignment No. 14682
 - gi No. 100611
 - % Identity 78.4
 - Alignment Length 111
 - Location of Alignment in SEQ ID NO 2297: from 1 to 110
 - Alignment No. 14683
 - gi No. 1076633
 - % Identity 88.3
 - Alignment Length 111
 - Location of Alignment in SEQ ID NO 2297: from 1 to 110
 - Alignment No. 14684
 - gi No. 1082205
 - % Identity 72.2
 - Alignment Length 108
 - Location of Alignment in SEQ ID NO 2297: from 2 to 109
 - Alignment No. 14685
 - gi No. 1216280
 - % Identity 89.2
 - Alignment Length 111
 - Location of Alignment in SEQ ID NO 2297: from 1 to 110
 - Alignment No. 14686
 - gi No. 1216285
 - % Identity 89.2
 - Alignment Length 111
 - Location of Alignment in SEQ ID NO 2297: from 1 to 110

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- Alignment No. 14687
- gi No. 134588
- % Identity 72.5
- Alignment Length 109
- Location of Alignment in SEQ ID NO 2297: from 1 to 109
- Alignment No. 14688
- gi No. 1362153
- % Identity 100
- Alignment Length 28
- Location of Alignment in SEQ ID NO 2297: from 1 to 28
- Alignment No. 14689
- gi No. 1362154
- % Identity 100
- Alignment Length 28
- Location of Alignment in SEQ ID NO 2297: from 1 to 28
- Alignment No. 14690
- gi No. 1362155
- % Identity 96.4
- Alignment Length 28
- Location of Alignment in SEQ ID NO 2297: from 1 to 28
- Alignment No. 14691
- gi No. 1477684
- % Identity 94.6
- Alignment Length 111
- Location of Alignment in SEQ ID NO 2297: from 1 to 110
- Alignment No. 14692
- gi No. 1703034
- % Identity 72.2
- Alignment Length 108
- Location of Alignment in SEQ ID NO 2297: from 2 to 109
- Alignment No. 14693
- gi No. 1729444
- % Identity 91
- Alignment Length 111
- Location of Alignment in SEQ ID NO 2297: from 1 to 110
- Alignment No. 14694
- gi No. 1742967
- % Identity 91
- Alignment Length 111
- Location of Alignment in SEQ ID NO 2297: from 1 to 110
- Alignment No. 14695
- gi No. 1743009
- % Identity 91
- Alignment Length 111
- Location of Alignment in SEQ ID NO 2297: from 1 to 110
- Alignment No. 14696
- gi No. 1935916
- % Identity 89.2
- Alignment Length 111
- Location of Alignment in SEQ ID NO 2297: from 1 to 110
- Alignment No. 14697
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- gi No. 2130048
- % Identity 96.4
- Alignment Length 111
- Location of Alignment in SEQ ID NO 2297: from 1 to 110
- Alignment No. 14698
- gi No. 2136044

- % Identity 75

- Alignment Length 32Location of Alignment in SEQ ID NO 2297: from 3 to 34
- Alignment No. 14699 - gi No. 2137442 - % Identity 94.1 - Alignment Length 34
- Location of Alignment in SEQ ID NO 2297: from 1 to 34
- Alignment No. 14700 - gi No. 2146759 - % Identity 100
- Alignment Length 28 Location of Alignment in SEQ ID NO 2297: from 1 to 28
- Alignment No. 14701 - gi No. 2146812 - % Identity 78.4 - Alignment Length 111
- Location of Alignment in SEQ ID NO 2297: from 1 to 110
- Alignment No. 14702 - gi No. 2274869 - % Identity 97.2 - Alignment Length 36 - Location of Alignme
- Location of Alignment in SEQ ID NO 2297: from 5 to 40
- Alignment No. 14703 - gi No. 2499626 - % Identity 72.5 - Alignment Length 109 - Location of Alignmen

- Alignment No. 14704 - gi No. 2507201 - % Identity 71.8

- Location of Alignment in SEQ ID NO 2297: from 1 to 109
- Alignment Length 110Location of Alignmen
- Location of Alignment in SEQ ID NO 2297: from 1 to 109
- Alignment No. 14705 - gi No. 3023235 - % Identity 86.7 - Alignment Length 30
- Location of Alignment in SEQ ID NO 2297: from 2 to 31
- Alignment No. 14706
- gi No. 322596
 % Identity 92.8
- Alignment Length 111
- Location of Alignment in SEQ ID NO 2297: from 1 to 110
- Alignment No. 14707
- gi No. 3341452

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- % Identity 79.3
- Alignment Length 111
- Location of Alignment in SEQ ID NO 2297: from 1 to 110
- Alignment No. 14708
- gi No. 400982
- % Identity 82.9
- Alignment Length 111
- Location of Alignment in SEQ ID NO 2297: from 1 to 110
- Alignment No. 14709
- gi No. 4091885
- % Identity 93.7
- Alignment Length 111
- Location of Alignment in SEQ ID NO 2297: from 1 to 110
- Alignment No. 14710
- gi No. 4099088
- % Identity 78.4
- Alignment Length 111
- Location of Alignment in SEQ ID NO 2297: from 1 to 110
- Alignment No. 14711
- gi No. 4107001
- % Identity 96.4
- Alignment Length 111
- Location of Alignment in SEQ ID NO 2297: from 1 to 110
- Alignment No. 14712
- gi No. 4107003
- % Identity 96.4
- Alignment Length 111
- Location of Alignment in SEQ ID NO 2297: from 1 to 110
- Alignment No. 14713
- gi No. 4107005
- % Identity 96.4
- Alignment Length 111
- Location of Alignment in SEQ ID NO 2297: from 1 to 110
- Alignment No. 14714
- gi No. 4107009
- % Identity 95.5
- Alignment Length 111
- Location of Alignment in SEQ ID NO 2297: from 1 to 110
- Alignment No. 14715
- qi No. 4432983
- % Identity 70
- Alignment Length 40
- Location of Alignment in SEQ ID NO 2297: from 8 to 47
- Alignment No. 14716
- gi No. 4520332
- % Identity 74.3
- Alignment Length 109
- Location of Alignment in SEQ ID NO 2297: from 1 to 109
- Alignment No. 14717
- gi No. 4567091
- % Identity 92.8

Attorney Docket No. 750-1097P Client Docket No. 80143.003

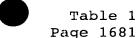


- Alignment Length 111
- Location of Alignment in SEQ ID NO 2297: from 1 to 110
- Alignment No. 14718
- gi No. 4982468
- % Identity 75.2
- Alignment Length 109
- Location of Alignment in SEQ ID NO 2297: from 2 to 110
- Alignment No. 14719
- gi No. 5410312
- % Identity 72.2
- Alignment Length 108
- Location of Alignment in SEQ ID NO 2297: from 2 to 109
- Alignment No. 14720
- gi No. 5442424
- % Identity 72.5
- Alignment Length 109
- Location of Alignment in SEQ ID NO 2297: from 1 to 109
- Alignment No. 14721
- gi No. 5453964
- % Identity 71.3
- Alignment Length 108
- Location of Alignment in SEQ ID NO 2297: from 2 to 109
- Alignment No. 14722
- gi No. 5453966
- % Identity 71.3
- Alignment Length 108
- Location of Alignment in SEQ ID NO 2297: from 2 to 109
- Alignment No. 14723
- gi No. 575292
- % Identity 96.4
- Alignment Length 111
- Location of Alignment in SEQ ID NO 2297: from 1 to 110
- Alignment No. 14724
- gi No. 728758
- % Identity 72.2
- Alignment Length 108
- Location of Alignment in SEQ ID NO 2297: from 2 to 109
- Alignment No. 14725
- gi No. 862473
- % Identity 72.2
- Alignment Length 108
- Location of Alignment in SEQ ID NO 2297: from 2 to 109
- (B) Polypeptide Sequence
 - Pat. Appln. SEQ ID NO 2298
 - Ceres seq_id 1502898
 - Location of start within SEQ ID NO 2296: at 2 nt.
- - (D) Related Amino Acid Sequences

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- (A) Polynucleotide Sequence
 - Pat. Appln. SEQ ID NO 2299
 - Ceres seq_id 1502902
 - (B) Polypeptide Sequence
 - Pat. Appln. SEQ ID NO 2300
 - Ceres seq_id 1502903
 - Location of start within SEQ ID NO 2299: at 1 nt.
- (C) Nomination and Annotation of Domains within Predicted Polypeptide(s) $\label{eq:condition} % \begin{array}{c} \text{Polyperiod} \\ \text{Poly$
 - (D) Related Amino Acid Sequences
 - Alignment No. 14726
 - gi No. 2160438
 - % Identity 72.7
 - Alignment Length 11
 - Location of Alignment in SEQ ID NO 2300: from 66 to 76
 - Alignment No. 14727
 - qi No. 286238
 - % Identity 72.7
 - Alignment Length 11
 - Location of Alignment in SEQ ID NO 2300: from 66 to 76
 - Alignment No. 14728
 - gi No. 348497
 - % Identity 72.7
 - Alignment Length 11
 - Location of Alignment in SEQ ID NO 2300: from 66 to 76
 - Alignment No. 14729
 - gi No. 548375
 - % Identity 72.7
 - Alignment Length 11
 - Location of Alignment in SEQ ID NO 2300: from 66 to 76
 - (B) Polypeptide Sequence
 - Pat. Appln. SEQ ID NO 2301
 - Ceres seq_id 1502904
 - Location of start within SEQ ID NO 2299: at 3 nt.
- - (D) Related Amino Acid Sequences
 - Alignment No. 14730
 - gi No. 3413810
 - % Identity 75
 - Alignment Length 12
 - Location of Alignment in SEQ ID NO 2301: from 26 to 37
 - (B) Polypeptide Sequence
 - Pat. Appln. SEQ ID NO 2302
 - Ceres seq_id 1502905
 - Location of start within SEQ ID NO 2299: at 46 nt.
- (C) Nomination and Annotation of Domains within Predicted Polypeptide(s)
 - (D) Related Amino Acid Sequences
 - Alignment No. 14731
 - gi No. 2160438
 - % Identity 72.7
 - Alignment Length 11

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- Location of Alignment in SEQ ID NO 2302: from 51 to 61
- Alignment No. 14732
- gi No. 286238
- % Identity 72.7
- Alignment Length 11
- Location of Alignment in SEQ ID NO 2302: from 51 to 61
- Alignment No. 14733
- qi No. 348497
- % Identity 72.7
- Alignment Length 11
- Location of Alignment in SEQ ID NO 2302: from 51 to 61
- Alignment No. 14734
- qi No. 548375
- % Identity 72.7
- Alignment Length 11
- Location of Alignment in SEQ ID NO 2302: from 51 to 61

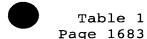
Maximum Length Sequence corresponding to clone ID 312920

- (A) Polynucleotide Sequence
 - Pat. Appln. SEQ ID NO 2303
 - Ceres seq_id 1502937
 - (B) Polypeptide Sequence
 - Pat. Appln. SEQ ID NO 2304
 - Ceres seq id 1502938
 - Location of start within SEQ ID NO 2303: at 1 nt.
- - (D) Related Amino Acid Sequences
 - Alignment No. 14735
 - gi No. 3367741
 - % Identity 75
 - Alignment Length 12
 - Location of Alignment in SEQ ID NO 2304: from 85 to 96
 - (B) Polypeptide Sequence
 - Pat. Appln. SEQ ID NO 2305
 - Ceres seq_id 1502939
 - Location of start within SEQ ID NO 2303: at 2 nt.
- (C) Nomination and Annotation of Domains within Predicted Polypeptide(s) $\label{eq:continuous} % \begin{array}{c} \text{Polypeptide}(s) \\ \text{Polypeptide}(s) \end{array}$
 - Alignment No. 14736
 - Nuclear transition protein 2
 - Location within SEQ ID NO 2305: from 7 to 72 aa.
 - (D) Related Amino Acid Sequences
 - (B) Polypeptide Sequence
 - Pat. Appln. SEQ ID NO 2306
 - Ceres seq_id 1502940
 - Location of start within SEQ ID NO 2303: at 3 nt.
- (C) Nomination and Annotation of Domains within Predicted Polypeptide(s)
 - (D) Related Amino Acid Sequences

Attorney Docket No. 750-1097P Client Docket No. 80143.003

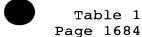
- (A) Polynucleotide Sequence
 - Pat. Appln. SEQ ID NO 2307
 - Ceres seq_id 1502981
 - (B) Polypeptide Sequence
 - Pat. Appln. SEQ ID NO 2308
 - Ceres seq id 1502982
 - Location of start within SEQ ID NO 2307: at 1 nt.
- - (D) Related Amino Acid Sequences
 - Alignment No. 14737
 - gi No. 465445
 - % Identity 71.4
 - Alignment Length 14
 - Location of Alignment in SEQ ID NO 2308: from 107 to 119
 - (B) Polypeptide Sequence
 - Pat. Appln. SEQ ID NO 2309
 - Ceres seq_id 1502983
 - Location of start within SEQ ID NO 2307: at 2 nt.
- - (D) Related Amino Acid Sequences
 - (B) Polypeptide Sequence
 - Pat. Appln. SEQ ID NO 2310
 - Ceres seq id 1502984
 - Location of start within SEQ ID NO 2307: at 3 nt.
- - (D) Related Amino Acid Sequences
 - Alignment No. 14738
 - gi No. 102706
 - % Identity 92.3
 - Alignment Length 13
 - Location of Alignment in SEQ ID NO 2310: from 106 to 118
 - Alignment No. 14739
 - gi No. 102706
 - % Identity 78.6
 - Alignment Length 14
 - Location of Alignment in SEQ ID NO 2310: from 106 to 119
 - Alignment No. 14740
 - gi Ño. 102706
 - % Identity 86.7
 - Alignment Length 15
 - Location of Alignment in SEQ ID NO 2310: from 106 to 119
 - Alignment No. 14741
 - gi No. 102706
 - % Identity 76.5
 - Alignment Length 17
 - Location of Alignment in SEQ ID NO 2310: from 106 to 119
 - Alignment No. 14742
 - gi No. 102707
 - % Identity 92.3

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- Alignment Length 13
- Location of Alignment in SEQ ID NO 2310: from 107 to 119
- Alignment No. 14743
- gi No. 1170389
- % Identity 85.7
- Alignment Length 14
- Location of Alignment in SEQ ID NO 2310: from 106 to 119
- Alignment No. 14744
- gi No. 1170392
- % Identity 85.7
- Alignment Length 14
- Location of Alignment in SEQ ID NO 2310: from 106 to 119
- Alignment No. 14745
- gi No. 1170396
- % Identity 70.6
- Alignment Length 17
- Location of Alignment in SEQ ID NO 2310: from 106 to 119
- Alignment No. 14746
- gi No. 1170397
- % Identity 70.6
- Alignment Length 17
- Location of Alignment in SEQ ID NO 2310: from 106 to 119
- Alignment No. 14747
- gi No. 1170398
- % Identity 70.6
- Alignment Length 17
- Location of Alignment in SEQ ID NO 2310: from 106 to 119
- Alignment No. 14748
- gi No. 1170401
- % Identity 78.6
- Alignment Length 14
- Location of Alignment in SEQ ID NO 2310: from 108 to 119
- Alignment No. 14749
- gi No. 1170405
- % Identity 85.7
- Alignment Length 14
- Location of Alignment in SEQ ID NO 2310: from 106 to 119
- Alignment No. 14750
- gi No. 1170406
- % Identity 85.7
- Alignment Length 14
- Location of Alignment in SEQ ID NO 2310: from 106 to 119
- Alignment No. 14751
- gi No. 123689
- % Identity 92.9
- Alignment Length 14
- Location of Alignment in SEQ ID NO 2310: from 106 to 119
- Alignment No. 14752
- gi No. 123689
- % Identity 82.4
- Alignment Length 17

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- Location of Alignment in SEQ ID NO 2310: from 106 to 122 - Alignment No. 14753 - gi No. 123695 - % Identity 92.3 - Alignment Length 13 - Location of Alignment in SEQ ID NO 2310: from 107 to 119 - Alignment No. 14754 - gi No. 131040 - % Identity 81.8 - Alignment Length 11 - Location of Alignment in SEQ ID NO 2310: from 107 to 117 - Alignment No. 14755 - gi No. 131040 - % Identity 81.8 - Alignment Length 11 - Location of Alignment in SEQ ID NO 2310: from 108 to 118 - Alignment No. 14756 - gi No. 131044 - % Identity 92.3 - Alignment Length 13 - Location of Alignment in SEQ ID NO 2310: from 106 to 118 - Alignment No. 14757 - gi No. 131044 - % Identity 78.6 - Alignment Length 14 - Location of Alignment in SEQ ID NO 2310: from 106 to 119 - Alignment No. 14758 - gi No. 131044 - % Identity 86.7 - Alignment Length 15 - Location of Alignment in SEQ ID NO 2310: from 106 to 119 - Alignment No. 14759 - gi No. 131044 - % Identity 76.5 - Alignment Length 17 - Location of Alignment in SEQ ID NO 2310: from 106 to 119 - Alignment No. 14760 - gi No. 163635 - % Identity 92.9 - Alignment Length 14 - Location of Alignment in SEQ ID NO 2310: from 106 to 119 - Alignment No. 14761 - gi No. 163635 - % Identity 85.7 - Alignment Length 14 - Location of Alignment in SEQ ID NO 2310: from 106 to 119 - Alignment No. 14762
- gi No. 163635
- % Identity 82.4
- Alignment Length 17
- Location of Alignment in SEQ ID NO 2310: from 106 to 122

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- Alignment No. 14763
          - gi No. 2134213
          - % Identity 92.3
          - Alignment Length 13
          - Location of Alignment in SEQ ID NO 2310: from 107 to 119
          - Alignment No. 14764
          - gi No. 2134213
          - % Identity 92.9
          - Alignment Length 14
          - Location of Alignment in SEQ ID NO 2310: from 106 to 119
          - Alignment No. 14765
          - gi No. 225057
          - % Identity 92.9
          - Alignment Length 14
          - Location of Alignment in SEQ ID NO 2310: from 106 to 119
          - Alignment No. 14766
          - gi No. 225057
          - % Identity 82.4
          - Alignment Length 17
          - Location of Alignment in SEQ ID NO 2310: from 106 to 122
          - Alignment No. 14767
          - gi No. 357984
          - % Identity 81.8
          - Alignment Length 11
          - Location of Alignment in SEQ ID NO 2310: from 108 to 118
          - Alignment No. 14768
          - gi No. 5456964
          - % Identity 76.9
          - Alignment Length 13
          - Location of Alignment in SEQ ID NO 2310: from 106 to 118
          - Alignment No. 14769
          - gi No. 85630
          - % Identity 81.8
          - Alignment Length 11
          - Location of Alignment in SEQ ID NO 2310: from 107 to 117
          - Alignment No. 14770
          - gi No. 85630
          - % Identity 81.8
          - Alignment Length 11
          - Location of Alignment in SEQ ID NO 2310: from 108 to 118
Maximum Length Sequence corresponding to clone ID 313054
(A) Polynucleotide Sequence
    - Pat. Appln. SEQ ID NO 2311
    - Ceres seq_id 1502985
   (B) Polypeptide Sequence
       - Pat. Appln. SEQ ID NO 2312
       - Ceres seq_id 1502986
       - Location of start within SEQ ID NO 2311: at 3 nt.
```

- (C) Nomination and Annotation of Domains within Predicted Polypeptide(s) $\label{eq:condition}$
 - Alignment No. 14771

13

- Assemblin (Peptidase family S21)
- Location within SEQ ID NO 2312: from 21 to 102 aa.
- (D) Related Amino Acid Sequences
- (B) Polypeptide Sequence
 - Pat. Appln. SEQ ID NO 2313
 - Ceres seq_id 1502987
 - Location of start within SEQ ID NO 2311: at 167 nt.
- (C) Nomination and Annotation of Domains within Predicted Polypeptide(s)
 - (D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 313104

- (A) Polynucleotide Sequence
 - Pat. Appln. SEQ ID NO 2314
 - Ceres seq id 1503000
 - (B) Polypeptide Sequence
 - Pat. Appln. SEQ ID NO 2315
 - Ceres seq_id 1503001
 - Location of start within SEQ ID NO 2314: at 1 nt.
- - (D) Related Amino Acid Sequences
 - (B) Polypeptide Sequence
 - Pat. Appln. SEQ ID NO 2316
 - Ceres seq_id 1503002
 - Location of start within SEQ ID NO 2314: at 2 nt.
- (C) Nomination and Annotation of Domains within Predicted Polypeptide(s) $% \left(\frac{1}{2}\right) =\frac{1}{2}\left(\frac{1}{2}\right) +\frac{1}{2}\left(\frac{1}{2}\right) +\frac{$
 - Alignment No. 14772
 - CRAL/TRIO domain.
 - Location within SEQ ID NO 2316: from 7 to 80 aa.
 - (D) Related Amino Acid Sequences

- (A) Polynucleotide Sequence
 - Pat. Appln. SEQ ID NO 2317
 - Ceres seq_id 1503010
 - (B) Polypeptide Sequence
 - Pat. Appln. SEQ ID NO 2318
 - Ceres seq_id 1503011
 - Location of start within SEQ ID NO 2317: at 2 nt.
- - Alignment No. 14773
 - Zinc finger, C3HC4 type (RING finger)
 - Location within SEO ID NO 2318: from 58 to 106 aa.
 - (D) Related Amino Acid Sequences
 - (B) Polypeptide Sequence
 - Pat. Appln. SEQ ID NO 2319
 - Ceres seq id 1503012
 - Location of start within SEQ ID NO 2317: at 77 nt.

- (C) Nomination and Annotation of Domains within Predicted Polypeptide(s) $% \left(\frac{1}{2}\right) =\frac{1}{2}\left(\frac{1}{2}\right) +\frac{1}{2}\left(\frac{1}{2}\right) +\frac{$
 - Alignment No. 14774
 - Zinc finger, C3HC4 type (RING finger)
 - Location within SEQ ID NO 2319: from 33 to 81 aa.
 - (D) Related Amino Acid Sequences

- (A) Polynucleotide Sequence
 - Pat. Appln. SEQ ID NO 2320
 - Ceres seq_id 1503042
 - (B) Polypeptide Sequence
 - Pat. Appln. SEQ ID NO 2321
 - Ceres seq_id 1503043
 - Location of start within SEQ ID NO 2320: at 1 nt.
- - (D) Related Amino Acid Sequences
 - Alignment No. 14775
 - gi No. 2529670
 - % Identity 81.3
 - Alignment Length 16
 - Location of Alignment in SEQ ID NO 2321: from 24 to 39
 - Alignment No. 14776
 - gi No. 3021348
 - % Identity 80
 - Alignment Length 15
 - Location of Alignment in SEQ ID NO 2321: from 26 to 40
 - (B) Polypeptide Sequence
 - Pat. Appln. SEQ ID NO 2322
 - Ceres seq_id 1503044
 - Location of start within SEQ ID NO 2320: at 67 nt.
- (C) Nomination and Annotation of Domains within Predicted Polypeptide(s) $% \left(\frac{1}{2}\right) =\frac{1}{2}\left(\frac{1}{2}\right) +\frac{1}{2}\left(\frac{1}{2}\right) +\frac{$
 - (D) Related Amino Acid Sequences
 - Alignment No. 14777
 - gi No. 2529670
 - % Identity 81.3
 - Alignment Length 16
 - Location of Alignment in SEQ ID NO 2322: from 2 to 17
 - Alignment No. 14778
 - gi No. 3021348
 - % Identity 80
 - Alignment Length 15
 - Location of Alignment in SEQ ID NO 2322: from 4 to 18
 - (B) Polypeptide Sequence
 - Pat. Appln. SEQ ID NO 2323
 - Ceres seq_id 1503045
 - Location of start within SEQ ID NO 2320: at 225 nt.
- - Alignment No. 14779

- Eukaryotic ribosomal protein L18
- Location within SEQ ID NO 2323: from 1 to 51 aa.
- (D) Related Amino Acid Sequences
 - Alignment No. 14780
 - gi No. 1172977
 - % Identity 72.3
 - Alignment Length 83
 - Location of Alignment in SEQ ID NO 2323: from 1 to 49
 - Alignment No. 14781
 - gi No. 2529670
 - % Identity 73.1
 - Alignment Length 78
 - Location of Alignment in SEQ ID NO 2323: from 1 to 44

- (A) Polynucleotide Sequence
 - Pat. Appln. SEQ ID NO 2324
 - Ceres seq_id 1503048
 - (B) Polypeptide Sequence
 - Pat. Appln. SEQ ID NO 2325
 - Ceres seq_id 1503049
 - Location of start within SEQ ID NO 2324: at 85 nt.
- (C) Nomination and Annotation of Domains within Predicted Polypeptide(s) $% \left(\frac{1}{2}\right) =\frac{1}{2}\left(\frac{1}{2}\right) +\frac{1}{2}\left(\frac{1}{2}\right) +\frac{$
 - (D) Related Amino Acid Sequences
 - Alignment No. 14782
 - gi No. 1171036
 - % Identity 75
 - Alignment Length 20
 - Location of Alignment in SEQ ID NO 2325: from 1 to 20
 - Alignment No. 14783
 - gi No. 1480016
 - % Identity 70
 - Alignment Length 20
 - Location of Alignment in SEQ ID NO 2325: from 1 to 20
 - Alignment No. 14784
 - gi No. 2407331
 - % Identity 75
 - Alignment Length 20
 - Location of Alignment in SEQ ID NO 2325: from 1 to 20
 - Alignment No. 14785
 - gi No. 2497887
 - % Identity 72.2
 - Alignment Length 18
 - Location of Alignment in SEQ ID NO 2325: from 1 to 18
 - Alignment No. 14786
 - gi No. 2497888
 - % Identity 77.8
 - Alignment Length 18
 - Location of Alignment in SEQ ID NO 2325: from 1 to 18
 - Alignment No. 14787
 - gi No. 2497890
 - % Identity 77.8

- Alignment Length 18
- Location of Alignment in SEQ ID NO 2325: from 1 to 18
- Alignment No. 14788
- gi No. 2497892
- % Identity 70
- Alignment Length 20
- Location of Alignment in SEQ ID NO 2325: from 1 to 20
- Alignment No. 14789
- gi No. 2497893
- % Identity 70
- Alignment Length 20
- Location of Alignment in SEQ ID NO 2325: from 1 to 20
- Alignment No. 14790
- gi No. 2497895
- % Identity 70
- Alignment Length 20
- Location of Alignment in SEQ ID NO 2325: from 1 to 20
- Alignment No. 14791
- gi No. 2497901
- % Identity 70
- Alignment Length 20
- Location of Alignment in SEQ ID NO 2325: from 1 to 20
- Alignment No. 14792
- gi No. 2497903
- % Identity 70
- Alignment Length 20
- Location of Alignment in SEQ ID NO 2325: from 1 to 20 $\,$
- Alignment No. 14793
- gi No. 2497904
- % Identity 75
- Alignment Length 20
- Location of Alignment in SEQ ID NO 2325: from 1 to 20
- Alignment No. 14794
- gi No. 2507587
- % Identity 70
- Alignment Length 20
- Location of Alignment in SEQ ID NO 2325: from 1 to 20
- Alignment No. 14795
- gi No. 266579
- % Identity 70
- Alignment Length 20
- Location of Alignment in SEQ ID NO 2325: from 1 to 20
- Alignment No. 14796
- gi No. 3694984
- % Identity 75
- Alignment Length 20
- Location of Alignment in SEQ ID NO 2325: from 1 to 20
- Alignment No. 14797
- gi No. 3900980
- % Identity 70
- Alignment Length 20

- Location of Alignment in SEQ ID NO 2325: from 1 to 20
- Alignment No. 14798
- gi No. 3901014
- % Identity 70
- Alignment Length 20
- Location of Alignment in SEQ ID NO 2325: from 1 to 20
- Alignment No. 14799
- gi No. 4877893
- % Identity 70
- Alignment Length 20
- Location of Alignment in SEQ ID NO 2325: from 1 to 20
- Alignment No. 14800
- gi No. 72178
- % Identity 70
- Alignment Length 20
- Location of Alignment in SEQ ID NO 2325: from 1 to 20

- (A) Polynucleotide Sequence
 - Pat. Appln. SEQ ID NO 2326
 - Ceres seq_id 1503064
 - (B) Polypeptide Sequence
 - Pat. Appln. SEQ ID NO 2327
 - Ceres seq_id 1503065
 - Location of start within SEQ ID NO 2326: at 1 nt.
- - Alignment No. 14801
 - Fatty acid desaturase
 - Location within SEQ ID NO 2327: from 37 to 128 aa.
 - (D) Related Amino Acid Sequences
 - Alignment No. 14802
 - gi No. 4104056
 - % Identity 71.7
 - Alignment Length 166
 - Location of Alignment in SEQ ID NO 2327: from 5 to 169
 - (B) Polypeptide Sequence
 - Pat. Appln. SEQ ID NO 2328
 - Ceres seq id 1503066
 - Location of start within SEQ ID NO 2326: at 3 nt.
- - (D) Related Amino Acid Sequences
 - Alignment No. 14803
 - gi No. 100214
 - % Identity 71.4
 - Alignment Length 15
 - Location of Alignment in SEQ ID NO 2328: from 2 to 15
 - Alignment No. 14804
 - gi No. 100214
 - % Identity 71.4
 - Alignment Length 15
 - Location of Alignment in SEQ ID NO 2328: from 2 to 15

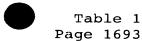
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- Alignment No. 14805
- gi No. 100214
- % Identity 71.4
- Alignment Length 15
 - Location of Alignment in SEQ ID NO 2328: from 2 to 15
- Alignment No. 14806
- gi No. 1185397
- % Identity 75
- Alignment Length 12
- Location of Alignment in SEQ ID NO 2328: from 4 to 15
- Alignment No. 14807
- gi No. 1185397
- % Identity 76.9
- Alignment Length 13
- Location of Alignment in SEQ ID NO 2328: from 3 to 15
- Alignment No. 14808
- gi No. 1185397
- % Identity 76.9
- Alignment Length 13
- Location of Alignment in SEQ ID NO 2328: from 3 to 15
- Alignment No. 14809
- gi No. 168237
- % Identity 71.4
- Alignment Length 14
- Location of Alignment in SEQ ID NO 2328: from 2 to 15
- Alignment No. 14810
- gi No. 2429362
- % Identity 72.7
- Alignment Length 11
- Location of Alignment in SEQ ID NO 2328: from 5 to 15
- Alignment No. 14811
- gi No. 4096360
- % Identity 75
- Alignment Length 12
- Location of Alignment in SEQ ID NO 2328: from 4 to 15
- Alignment No. 14812
- gi No. 4096360
- % Identity 76.9
- Alignment Length 13
- Location of Alignment in SEQ ID NO 2328: from 3 to 15
- Alignment No. 14813
- gi No. 4096360
- % Identity 76.9
- Alignment Length 13
- Location of Alignment in SEQ ID NO 2328: from 3 to 15
- Alignment No. 14814
- gi No. 5430752
- % Identity 71.4
- Alignment Length 14
- Location of Alignment in SEQ ID NO 2328: from 2 to 15
```

- (B) Polypeptide Sequence
 - Pat. Appln. SEQ ID NO 2329
 - Ceres seq_id 1503067
 - Location of start within SEQ ID NO 2326: at 115 nt.
- (C) Nomination and Annotation of Domains within Predicted Polypeptide(s)
 - Alignment No. 14815
 - Fatty acid desaturase
 - Location within SEQ ID NO 2329: from 1 to 90 aa.
 - (D) Related Amino Acid Sequences
 - Alignment No. 14816
 - gi No. 4104056
 - % Identity 71.7
 - Alignment Length 166
 - Location of Alignment in SEQ ID NO 2329: from 1 to 131

- (A) Polynucleotide Sequence
 - Pat. Appln. SEQ ID NO 2330
 - Ceres seq_id 1503071
 - (B) Polypeptide Sequence
 - Pat. Appln. SEQ ID NO 2331
 - Ceres seq_id 1503072
 - Location of start within SEQ ID NO 2330: at 1 nt.
- (C) Nomination and Annotation of Domains within Predicted Polypeptide(s)
 - (D) Related Amino Acid Sequences
 - Alignment No. 14817
 - gi No. 3850569
 - % Identity 73.1
 - Alignment Length 26
 - Location of Alignment in SEQ ID NO 2331: from 16 to 41
 - (B) Polypeptide Sequence
 - Pat. Appln. SEQ ID NO 2332
 - Ceres seq id 1503073
 - Location of start within SEQ ID NO 2330: at 147 nt.
- (C) Nomination and Annotation of Domains within Predicted Polypeptide(s) $\,$
 - (D) Related Amino Acid Sequences

- (A) Polynucleotide Sequence
 - Pat. Appln. SEQ ID NO 2333
 - Ceres seq_id 1503104
 - (B) Polypeptide Sequence
 - Pat. Appln. SEQ ID NO 2334
 - Ceres seq_id 1503105
 - Location of start within SEQ ID NO 2333: at 1 nt.
- - (D) Related Amino Acid Sequences
 - Alignment No. 14818
 - gi No. 2564066
 - % Identity 78.5
 - Alignment Length 65

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- Location of Alignment in SEQ ID NO 2334: from 38 to 102
- Alignment No. 14819
- gi No. 5031275
- % Identity 70.8
- Alignment Length 65
- Location of Alignment in SEQ ID NO 2334: from 38 to 102
- (B) Polypeptide Sequence
 - Pat. Appln. SEQ ID NO 2335
 - Ceres seq_id 1503106
 - Location of start within SEQ ID NO 2333: at 112 nt.
- - (D) Related Amino Acid Sequences
 - Alignment No. 14820
 - gi No. 2564066
 - % Identity 78.5
 - Alignment Length 65
 - Location of Alignment in SEQ ID NO 2335: from 1 to 65
 - Alignment No. 14821
 - gi No. 5031275
 - % Identity 70.8
 - Alignment Length 65
 - Location of Alignment in SEQ ID NO 2335: from 1 to 65
 - (B) Polypeptide Sequence
 - Pat. Appln. SEQ ID NO 2336
 - Ceres seq_id 1503107
 - Location of start within SEQ ID NO 2333: at 222 nt.
- (C) Nomination and Annotation of Domains within Predicted Polypeptide(s)
 - (D) Related Amino Acid Sequences
 - Alignment No. 14822
 - gi No. 2464905
 - % Identity 77.8
 - Alignment Length 36
 - Location of Alignment in SEQ ID NO 2336: from 29 to 63
 - Alignment No. 14823
 - gi No. 2564066
 - % Identity 83.8
 - Alignment Length 37
 - Location of Alignment in SEQ ID NO 2336: from 28 to 63
 - Alignment No. 14824
 - gi No. 3269288
 - % Identity 86.5
 - Alignment Length 37
 - Location of Alignment in SEQ ID NO 2336: from 28 to 63
 - Alignment No. 14825
 - gi No. 5031275
 - % Identity 83.8
 - Alignment Length 37
 - Location of Alignment in SEQ ID NO 2336: from 28 to 63

- (A) Polynucleotide Sequence
 - Pat. Appln. SEQ ID NO 2337
 - Ceres seq_id 1503108
 - (B) Polypeptide Sequence
 - Pat. Appln. SEQ ID NO 2338
 - Ceres seq_id 1503109
 - Location of start within SEQ ID NO 2337: at 3 nt.
- (C) Nomination and Annotation of Domains within Predicted Polypeptide(s) $\label{eq:condition} % \begin{array}{c} \text{Polyperiod} \\ \text{Poly$
 - Alignment No. 14826
 - Eukaryotic protein kinase domain
 - Location within SEQ ID NO 2338: from 38 to 145 aa.
 - (D) Related Amino Acid Sequences
 - Alignment No. 14827
 - gi No. 1161254
 - % Identity 83.6
 - Alignment Length 110
 - Location of Alignment in SEQ ID NO 2338: from 36 to 145
 - Alignment No. 14828
 - gi No. 1168529
 - % Identity 80.9
 - Alignment Length 110
 - Location of Alignment in SEQ ID NO 2338: from 36 to 145
 - Alignment No. 14829
 - gi No. 1168530
 - % Identity 77.3
 - Alignment Length 110
 - Location of Alignment in SEQ ID NO 2338: from 36 to 145
 - Alignment No. 14830
 - gi No. 1362002
 - % Identity 77.6
 - Alignment Length 116
 - Location of Alignment in SEQ ID NO 2338: from 31 to 145
 - Alignment No. 14831
 - gi No. 1362026
 - % Identity 80
 - Alignment Length 110
 - Location of Alignment in SEQ ID NO 2338: from 36 to 145
 - Alignment No. 14832
 - gi No. 1362050
 - % Identity 83
 - Alignment Length 112
 - Location of Alignment in SEQ ID NO 2338: from 34 to 145
 - Alignment No. 14833
 - gi No. 1362051
 - % Identity 84.5
 - Alignment Length 110
 - Location of Alignment in SEQ ID NO 2338: from 36 to 145
 - Alignment No. 14834
 - gi No. 1669573
 - % Identity 93.8
 - Alignment Length 112

- Location of Alignment in SEQ ID NO 2338: from 34 to 145
- Alignment No. 14835
- gi No. 1944000
- % Identity 93.8
- Alignment Length 112
- Location of Alignment in SEQ ID NO 2338: from 34 to 145
- Alignment No. 14836
- gi No. 2055374
- % Identity 76.4
- Alignment Length 110
- Location of Alignment in SEQ ID NO 2338: from 36 to 145
- Alignment No. 14837
- gi No. 2129803
- % Identity 81.8
- Alignment Length 110
- Location of Alignment in SEQ ID NO 2338: from 36 to 145
- Alignment No. 14838
- gi No. 2146746
- % Identity 77.6
- Alignment Length 116
- Location of Alignment in SEQ ID NO 2338: from 31 to 145
- Alignment No. 14839
- gi No. 3046731
- % Identity 81.8
- Alignment Length 110
- Location of Alignment in SEQ ID NO 2338: from 36 to 145
- Alignment No. 14840
- gi No. 310580
- % Identity 82.1
- Alignment Length 112
- Location of Alignment in SEQ ID NO 2338: from 34 to 145
- Alignment No. 14841
- gi No. 3169176
- % Identity 75.2
- Alignment Length 113
- Location of Alignment in SEQ ID NO 2338: from 36 to 148
- Alignment No. 14842
- gi No. 3297819
- % Identity 78.4
- Alignment Length 116
- Location of Alignment in SEQ ID NO 2338: from 31 to 145
- Alignment No. 14843
- gi No. 3811293
- % Identity 84.8
- Alignment Length 112
- Location of Alignment in SEQ ID NO 2338: from 34 to 145
- Alignment No. 14844
- gi No. 4098174
- % Identity 85.7
- Alignment Length 112
- Location of Alignment in SEQ ID NO 2338: from 34 to 145

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- Alignment No. 14845
- gi No. 416564
- % Identity 80.2
- Alignment Length 101
- Location of Alignment in SEQ ID NO 2338: from 45 to 145
- Alignment No. 14846
- gi No. 4490752
- % Identity 76.4
- Alignment Length 110
- Location of Alignment in SEQ ID NO 2338: from 36 to 145
- Alignment No. 14847
- gi No. 481002
- % Identity 74.5
- Alignment Length 110
- Location of Alignment in SEQ ID NO 2338: from 36 to 145
- (B) Polypeptide Sequence
 - Pat. Appln. SEQ ID NO 2339
 - Ceres seq_id 1503110
 - Location of start within SEQ ID NO 2337: at 102 nt.
- (C) Nomination and Annotation of Domains within Predicted Polypeptide(s)
 - Alignment No. 14848
 - Eukaryotic protein kinase domain
 - Location within SEQ ID NO 2339: from 5 to 112 aa.
 - (D) Related Amino Acid Sequences
 - Alignment No. 14849
 - gi No. 1161254
 - % Identity 83.6
 - Alignment Length 110
 - Location of Alignment in SEQ ID NO 2339: from 3 to 112
 - Alignment No. 14850
 - gi No. 1168529
 - % Identity 80.9
 - Alignment Length 110
 - Location of Alignment in SEQ ID NO 2339: from 3 to 112
 - Alignment No. 14851
 - gi No. 1168530
 - % Identity 77.3
 - Alignment Length 110
 - Location of Alignment in SEQ ID NO 2339: from 3 to 112
 - Alignment No. 14852
 - gi No. 1362002
 - % Identity 77.6
 - Alignment Length 116
 - Location of Alignment in SEQ ID NO 2339: from 1 to 112
 - Alignment No. 14853
 - gi No. 1362026
 - % Identity 80
 - Alignment Length 110
 - Location of Alignment in SEQ ID NO 2339: from 3 to 112

- Alignment No. 14854 - gi No. 1362050 - % Identity 83 - Alignment Length 112 - Location of Alignment in SEQ ID NO 2339: from 1 to 112 - Alignment No. 14855 - gi No. 1362051 - % Identity 84.5 - Alignment Length 110 - Location of Alignment in SEQ ID NO 2339: from 3 to 112 - Alignment No. 14856 - gi No. 1669573 - % Identity 93.8 - Alignment Length 112 - Location of Alignment in SEQ ID NO 2339: from 1 to 112 $\,$ - Alignment No. 14857 - gi No. 1944000 - % Identity 93.8 - Alignment Length 112 - Location of Alignment in SEQ ID NO 2339: from 1 to 112 - Alignment No. 14858 - gi No. 2055374 - % Identity 76.4 - Alignment Length 110 - Location of Alignment in SEQ ID NO 2339: from 3 to 112 - Alignment No. 14859 - gi No. 2129803 - % Identity 81.8 - Alignment Length 110 - Location of Alignment in SEQ ID NO 2339: from 3 to 112 - Alignment No. 14860 - gi No. 2146746 - % Identity 77.6 - Alignment Length 116 - Location of Alignment in SEQ ID NO 2339: from 1 to 112 - Alignment No. 14861 - gi No. 3046731 - % Identity 81.8 - Alignment Length 110 - Location of Alignment in SEQ ID NO 2339: from 3 to 112 - Alignment No. 14862 - gi No. 310580 - % Identity 82.1 - Alignment Length 112 - Location of Alignment in SEQ ID NO 2339: from 1 to 112 - Alignment No. 14863 - gi No. 3169176 - % Identity 75.2

- Location of Alignment in SEQ ID NO 2339: from 3 to 115

- Alignment No. 14864

- Alignment Length 113

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- gi No. 3297819
- % Identity 78.4
- Alignment Length 116
- Location of Alignmen
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- Location of Alignment in SEQ ID NO 2339: from 1 to 112
- Alignment No. 14865
- gi No. 3811293
- % Identity 84.8
- Alignment Length 112
- Location of Alignment in SEQ ID NO 2339: from 1 to 112
- Alignment No. 14866
- gi No. 4098174
- % Identity 85.7
- Alignment Length 112
- Location of Alignment in SEQ ID NO 2339: from 1 to 112
- Alignment No. 14867
- qi No. 416564
- % Identity 80.2
- Alignment Length 101
- Location of Alignment in SEQ ID NO 2339: from 12 to 112
- Alignment No. 14868
- gi No. 4490752
- % Identity 76.4
- Alignment Length 110
- Location of Alignment in SEQ ID NO 2339: from 3 to 112
- Alignment No. 14869
- gi No. 481002
- % Identity 74.5
- Alignment Length 110
- Location of Alignment in SEQ ID NO 2339: from 3 to 112

- (A) Polynucleotide Sequence
 - Pat. Appln. SEQ ID NO 2340
 - Ceres seq id 1503132
 - (B) Polypeptide Sequence
 - Pat. Appln. SEQ ID NO 2341
 - Ceres seq_id 1503133
 - Location of start within SEQ ID NO 2340: at 1 nt.
- (C) Nomination and Annotation of Domains within Predicted Polypeptide(s) $\label{eq:condition} % \begin{array}{c} \text{Polyperiod} \\ \text{Poly$
 - (D) Related Amino Acid Sequences
 - (B) Polypeptide Sequence
 - Pat. Appln. SEQ ID NO 2342
 - Ceres seq id 1503134
 - Location of start within SEQ ID NO 2340: at 80 nt.
- - (D) Related Amino Acid Sequences
 - Alignment No. 14870
 - gi No. 547305
 - % Identity 70
 - Alignment Length 20
 - Location of Alignment in SEQ ID NO 2342: from 32 to 51

- (B) Polypeptide Sequence
 - Pat. Appln. SEQ ID NO 2343
 - Ceres seq_id 1503135
 - Location of start within SEQ ID NO 2340: at 122 nt.
- (C) Nomination and Annotation of Domains within Predicted Polypeptide(s) $% \left(\frac{1}{2}\right) =\frac{1}{2}\left(\frac{1}{2}\right) +\frac{1}{2}\left(\frac{1}{2}\right) +\frac{$
 - (D) Related Amino Acid Sequences
 - Alignment No. 14871
 - gi No. 547305
 - % Identity 70
 - Alignment Length 20
 - Location of Alignment in SEQ ID NO 2343: from 18 to 37

- (A) Polynucleotide Sequence
 - Pat. Appln. SEQ ID NO 2344
 - Ceres seq id 1503136
 - (B) Polypeptide Sequence
 - Pat. Appln. SEQ ID NO 2345
 - Ceres seq_id 1503137
 - Location of start within SEQ ID NO 2344: at 2 nt.
- (C) Nomination and Annotation of Domains within Predicted Polypeptide(s) $% \left(\frac{1}{2}\right) =\frac{1}{2}\left(\frac{1}{2}\right) +\frac{1}{2}\left(\frac{1}{2}\right) +\frac{$
 - (D) Related Amino Acid Sequences
 - Alignment No. 14872
 - gi No. 103026
 - % Identity 72.7
 - Alignment Length 11
 - Location of Alignment in SEQ ID NO 2345: from 4 to 14
 - (B) Polypeptide Sequence
 - Pat. Appln. SEQ ID NO 2346
 - Ceres seq_id 1503138
 - Location of start within SEQ ID NO 2344: at 3 nt.
- (C) Nomination and Annotation of Domains within Predicted Polypeptide(s) $% \left(\frac{1}{2}\right) =\frac{1}{2}\left(\frac{1}{2}\right) +\frac{1}{2}\left(\frac{1}{2}\right) +\frac{$
 - (D) Related Amino Acid Sequences
 - Alignment No. 14873
 - gi No. 1869859
 - % Identity 75
 - Alignment Length 12
 - Location of Alignment in SEQ ID NO 2346: from 64 to 75
 - (B) Polypeptide Sequence
 - Pat. Appln. SEQ ID NO 2347
 - Ceres seq_id 1503139
 - Location of start within SEQ ID NO 2344: at 42 nt.
- (C) Nomination and Annotation of Domains within Predicted Polypeptide(s) $% \left(\frac{1}{2}\right) =\frac{1}{2}\left(\frac{1}{2}\right) +\frac{1}{2}\left(\frac{1}{2}\right) +\frac{$
 - (D) Related Amino Acid Sequences
 - Alignment No. 14874
 - gi No. 1869859
 - % Identity 75
 - Alignment Length 12
 - Location of Alignment in SEQ ID NO 2347: from 51 to 62

- (A) Polynucleotide Sequence
 - Pat. Appln. SEQ ID NO 2348
 - Ceres seq id 1503144
 - (B) Polypeptide Sequence
 - Pat. Appln. SEQ ID NO 2349
 - Ceres seq id 1503145
 - Location of start within SEQ ID NO 2348: at 2 nt.
- - (D) Related Amino Acid Sequences
 - Alignment No. 14875
 - gi No. 3426262
 - % Identity 72.8
 - Alignment Length 81
 - Location of Alignment in SEQ ID NO 2349: from 28 to 108
 - (B) Polypeptide Sequence
 - Pat. Appln. SEQ ID NO 2350
 - Ceres seq_id 1503146
 - Location of start within SEQ ID NO 2348: at 20 nt.
- - (D) Related Amino Acid Sequences
 - Alignment No. 14876
 - gi No. 3426262
 - % Identity 72.8
 - Alignment Length 81
 - Location of Alignment in SEQ ID NO 2350: from 22 to 102
 - (B) Polypeptide Sequence
 - Pat. Appln. SEQ ID NO 2351
 - Ceres seq_id 1503147
 - Location of start within SEQ ID NO 2348: at 137 nt.
- (C) Nomination and Annotation of Domains within Predicted Polypeptide(s) $\label{eq:polypeptide} % \begin{array}{c} (C) & (C$
 - (D) Related Amino Acid Sequences
 - Alignment No. 14877
 - gi No. 3426262
 - % Identity 72.8
 - Alignment Length 81
 - Location of Alignment in SEQ ID NO 2351: from 1 to 63

- (A) Polynucleotide Sequence
 - Pat. Appln. SEQ ID NO 2352
 - Ceres seq_id 1503148
 - (B) Polypeptide Sequence
 - Pat. Appln. SEQ ID NO 2353
 - Ceres seq_id 1503149
 - Location of start within SEQ ID NO 2352: at 1 nt.
- - (D) Related Amino Acid Sequences
 - Alignment No. 14878
 - gi No. 1351999
 - % Identity 81

- Alignment Length 21
- Location of Alignment in SEQ ID NO 2353: from 1 to 21
- Alignment No. 14879
- gi No. 2129613
- % Identity 78.3
- Alignment Length 23
- Location of Alignment in SEQ ID NO 2353: from 1 to 23
- Alignment No. 14880
- gi No. 3096930
- % Identity 89.5
- Alignment Length 19
- Location of Alignment in SEQ ID NO 2353: from 1 to 19
- Alignment No. 14881
- gi No. 4510417
- % Identity 77.3
- Alignment Length 22
- Location of Alignment in SEQ ID NO 2353: from 1 to 22
- Alignment No. 14882
- gi No. 4544389
- % Identity 94.7
- Alignment Length 19
- Location of Alignment in SEQ ID NO 2353: from 1 to 19
- Alignment No. 14883
- gi No. 5678605
- % Identity 76
- Alignment Length 25
- Location of Alignment in SEQ ID NO 2353: from 1 to 25
- (B) Polypeptide Sequence
 - Pat. Appln. SEQ ID NO 2354
 - Ceres seq_id 1503150
 - Location of start within SEQ ID NO 2352: at 3 nt.
- - (D) Related Amino Acid Sequences

- (A) Polynucleotide Sequence
 - Pat. Appln. SEQ ID NO 2355
 - Ceres seq_id 1503151
 - (B) Polypeptide Sequence
 - Pat. Appln. SEQ ID NO 2356
 - Ceres seq_id 1503152
 - Location of start within SEQ ID NO 2355: at 1 nt.
- (C) Nomination and Annotation of Domains within Predicted Polypeptide(s)
 - (D) Related Amino Acid Sequences
 - (B) Polypeptide Sequence
 - Pat. Appln. SEQ ID NO 2357
 - Ceres seq_id 1503153
 - Location of start within SEQ ID NO 2355: at 2 nt.

- (C) Nomination and Annotation of Domains within Predicted Polypeptide(s)
 - (D) Related Amino Acid Sequences
 - (B) Polypeptide Sequence
 - Pat. Appln. SEQ ID NO 2358
 - Ceres seq_id 1503154
 - Location of start within SEQ ID NO 2355: at 3 nt.
- (C) Nomination and Annotation of Domains within Predicted Polypeptide(s) $% \left(\frac{1}{2}\right) =\frac{1}{2}\left(\frac{1}{2}\right) +\frac{1}{2}\left(\frac{1}{2}\right) +\frac{$
 - Alignment No. 14884
 - 7 transmembrane receptor (rhodopsin family)
 - Location within SEQ ID NO 2358: from 5 to 95 aa.
 - (D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 313590 (A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 2359
- Ceres seq_id 1503160
- (B) Polypeptide Sequence
 - Pat. Appln. SEQ ID NO 2360
 - Ceres seq_id 1503161
 - Location of start within SEQ ID NO 2359: at 1 nt.
- (C) Nomination and Annotation of Domains within Predicted Polypeptide(s) $\dot{\ }$
 - (D) Related Amino Acid Sequences
 - Alignment No. 14885
 - gi No. 5689238
 - % Identity 75
 - Alignment Length 44
 - Location of Alignment in SEQ ID NO 2360: from 108 to 150

- (A) Polynucleotide Sequence
 - Pat. Appln. SEQ ID NO 2361
 - Ceres seq_id 1503170
 - (B) Polypeptide Sequence
 - Pat. Appln. SEQ ID NO 2362
 - Ceres seq_id 1503171
 - Location of start within SEQ ID NO 2361: at 3 nt.
- - Alignment No. 14886
 - Integrase
 - Location within SEQ ID NO 2362: from 58 to 125 aa.
 - (D) Related Amino Acid Sequences
 - (B) Polypeptide Sequence
 - Pat. Appln. SEQ ID NO 2363
 - Ceres seq_id 1503172
 - Location of start within SEQ ID NO 2361: at 3 nt.
- - Alignment No. 14887
 - Integrase

- - Location within SEQ ID NO 2363: from 58 to 125 aa.
- (D) Related Amino Acid Sequences

- (A) Polynucleotide Sequence
 - Pat. Appln. SEQ ID NO 2364
 - Ceres seq_id 1503191
 - (B) Polypeptide Sequence
 - Pat. Appln. SEQ ID NO 2365
 - Ceres seq_id 1503192
 - Location of start within SEQ ID NO 2364: at 37 nt.
- (C) Nomination and Annotation of Domains within Predicted Polypeptide(s) $\label{eq:condition} % \begin{array}{c} (C) & (C)$
 - (D) Related Amino Acid Sequences
 - Alignment No. 14888
 - gi No. 102707
 - % Identity 75
 - Alignment Length 12
 - Location of Alignment in SEQ ID NO 2365: from 115 to 126
 - Alignment No. 14889
 - gi No. 3153821
 - % Identity 71.4
 - Alignment Length 14
 - Location of Alignment in SEQ ID NO 2365: from 13 to 26
 - Alignment No. 14890
 - gi No. 5032119
 - % Identity 71.4
 - Alignment Length 14
 - Location of Alignment in SEQ ID NO 2365: from 13 to 26
 - (B) Polypeptide Sequence
 - Pat. Appln. SEQ ID NO 2366
 - Ceres seq_id 1503193
 - Location of start within SEQ ID NO 2364: at 134 nt.
- (C) Nomination and Annotation of Domains within Predicted Polypeptide(s) $% \left(1\right) =\left(1\right) \left(1\right) +\left(1\right) \left(1\right) \left(1\right) +\left(1\right) \left(1\right)$
 - (D) Related Amino Acid Sequences

- (A) Polynucleotide Sequence
 - Pat. Appln. SEQ ID NO 2367
 - Ceres seq id 1503200
 - (B) Polypeptide Sequence
 - Pat. Appln. SEQ ID NO 2368
 - Ceres seq_id 1503201
 - Location of start within SEQ ID NO 2367: at 1 nt.
- (C) Nomination and Annotation of Domains within Predicted Polypeptide(s) $% \left(\frac{1}{2}\right) =\frac{1}{2}\left(\frac{1}{2}\right) +\frac{1}{2}\left(\frac{1}{2}\right) +\frac{$
 - Alignment No. 14891
 - DEAD/DEAH box helicase
 - Location within SEQ ID NO 2368: from 73 to 151 aa.
 - (D) Related Amino Acid Sequences
 - (B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2369
- Ceres seq_id 1503202
- Location of start within SEQ ID NO 2367: at 1 nt.
- - Alignment No. 14892
 - DEAD/DEAH box helicase
 - Location within SEQ ID NO 2369: from 73 to 151 aa.
 - (D) Related Amino Acid Sequences
 - (B) Polypeptide Sequence
 - Pat. Appln. SEQ ID NO 2370
 - Ceres seq_id 1503203
 - Location of start within SEQ ID NO 2367: at 106 nt.
- (C) Nomination and Annotation of Domains within Predicted Polypeptide(s)
 - Alignment No. 14893
 - DEAD/DEAH box helicase
 - Location within SEQ ID NO 2370: from 38 to 116 aa.
 - (D) Related Amino Acid Sequences

- (A) Polynucleotide Sequence
 - Pat. Appln. SEQ ID NO 2371
 - Ceres seq_id 1503237
 - (B) Polypeptide Sequence
 - Pat. Appln. SEQ ID NO 2372
 - Ceres seq_id 1503238
 - Location of start within SEQ ID NO 2371: at 1 nt.
- - (D) Related Amino Acid Sequences
 - Alignment No. 14894
 - gi No. 1710490
 - % Identity 78.9
 - Alignment Length 19
 - Location of Alignment in SEQ ID NO 2372: from 22 to 40
 - Alignment No. 14895
 - qi No. 2245098
 - % Identity 94.1
 - Alignment Length 17
 - Location of Alignment in SEQ ID NO 2372: from 24 to 40
 - Alignment No. 14896
 - gi No. 2982249
 - % Identity 78.9
 - Alignment Length 19
 - Location of Alignment in SEQ ID NO 2372: from 22 to 40
 - Alignment No. 14897
 - gi No. 2982318
 - % Identity 78.9
 - Alignment Length 19
 - Location of Alignment in SEQ ID NO 2372: from 22 to 40

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- Alignment No. 14898
- gi No. 3122673
- % Identity 94.7
- Alignment Length 19
- Location of Alignment in SEQ ID NO 2372: from 22 to 40
- Alignment No. 14899
- gi No. 3608479
- % Identity 89.5
- Alignment Length 19
- Location of Alignment in SEQ ID NO 2372: from 22 to 40
- Alignment No. 14900
- gi No. 4506593
- % Identity 84.2
- Alignment Length 19
- Location of Alignment in SEQ ID NO 2372: from 22 to 40
- Alignment No. 14901
- gi No. 730532
- % Identity 84.2
- Alignment Length 19
- Location of Alignment in SEQ ID NO 2372: from 22 to 40
- Alignment No. 14902
- gi No. 730533
- % Identity 84.2
- Alignment Length 19
- Location of Alignment in SEQ ID NO 2372: from 22 to 40
- (B) Polypeptide Sequence
 - Pat. Appln. SEQ ID NO 2373
 - Ceres seq_id 1503239
 - Location of start within SEQ ID NO 2371: at 3 nt.
- - (D) Related Amino Acid Sequences
 - (B) Polypeptide Sequence
 - Pat. Appln. SEQ ID NO 2374
 - Ceres seq_id 1503240
 - Location of start within SEQ ID NO 2371: at 64 nt.
- - (D) Related Amino Acid Sequences
 - Alignment No. 14903
 - gi No. 1710490
 - % Identity 78.9
 - Alignment Length 19
 - Location of Alignment in SEQ ID NO 2374: from 1 to 19
 - Alignment No. 14904
 - gi No. 2245098
 - % Identity 94.1
 - Alignment Length 17
 - Location of Alignment in SEQ ID NO 2374: from 3 to 19
 - Alignment No. 14905
 - gi No. 2982249

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- % Identity 78.9
- Alignment Length 19
- Location of Alignment in SEQ ID NO 2374: from 1 to 19
- Alignment No. 14906
- qi No. 2982318
- % Identity 78.9
- Alignment Length 19
- Location of Alignment in SEQ ID NO 2374: from 1 to 19
- Alignment No. 14907
- gi No. 3122673
- % Identity 94.7
- Alignment Length 19
- Location of Alignment in SEQ ID NO 2374: from 1 to 19
- Alignment No. 14908
- gi No. 3608479
- % Identity 89.5
- Alignment Length 19
- Location of Alignment in SEQ ID NO 2374: from 1 to 19
- Alignment No. 14909
- qi No. 4506593
- % Identity 84.2
- Alignment Length 19
- Location of Alignment in SEQ ID NO 2374: from 1 to 19
- Alignment No. 14910
- gi No. 730532
- % Identity 84.2
- Alignment Length 19
- Location of Alignment in SEQ ID NO 2374: from 1 to 19
- Alignment No. 14911
- gi No. 730533
- % Identity 84.2
- Alignment Length 19
- Location of Alignment in SEQ ID NO 2374: from 1 to 19

- (A) Polynucleotide Sequence
 - Pat. Appln. SEQ ID NO 2375
 - Ceres seq_id 1503268
 - (B) Polypeptide Sequence
 - Pat. Appln. SEQ ID NO 2376
 - Ceres seq_id 1503269
 - Location of start within SEQ ID NO 2375: at 197 nt.
- - (D) Related Amino Acid Sequences
 - Alignment No. 14912
 - gi No. 2062167
 - % Identity 74.4
 - Alignment Length 39
 - Location of Alignment in SEQ ID NO 2376: from 24 to 62
 - (B) Polypeptide Sequence
 - Pat. Appln. SEQ ID NO 2377
 - Ceres seq id 1503270

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 - Location of start within SEO ID NO 2375: at 266 nt.
- (C) Nomination and Annotation of Domains within Predicted Polypeptide(s)
 - (D) Related Amino Acid Sequences
 - Alignment No. 14913
 - gi No. 2062167
 - % Identity 74.4
 - Alignment Length 39
 - Location of Alignment in SEQ ID NO 2377: from 1 to 39

- (A) Polynucleotide Sequence
 - Pat. Appln. SEQ ID NO 2378
 - Ceres seq_id 1503275
 - (B) Polypeptide Sequence
 - Pat. Appln. SEQ ID NO 2379
 - Ceres seq_id 1503276
 - Location of start within SEQ ID NO 2378: at 1 nt.
- (C) Nomination and Annotation of Domains within Predicted Polypeptide(s)
 - (D) Related Amino Acid Sequences
 - Alignment No. 14914
 - gi No. 1174492
 - % Identity 76.2
 - Alignment Length 42
 - Location of Alignment in SEQ ID NO 2379: from 42 to 83
 - Alignment No. 14915
 - gi No. 2494300
 - % Identity 76.2
 - Alignment Length 42
 - Location of Alignment in SEQ ID NO 2379: from 42 to 83
 - Alignment No. 14916
 - gi No. 2832707
 - % Identity 81
 - Alignment Length 42
 - Location of Alignment in SEQ ID NO 2379: from 42 to 83
 - Alignment No. 14917
 - gi No. 3142294
 - % Identity 78.3
 - Alignment Length 46
 - Location of Alignment in SEQ ID NO 2379: from 39 to 83
 - Alignment No. 14918
 - gi No. 3790165
 - % Identity 72.5
 - Alignment Length 40
 - Location of Alignment in SEQ ID NO 2379: from 44 to 83
 - Alignment No. 14919
 - gi No. 3790184
 - % Identity 75
 - Alignment Length 40
 - Location of Alignment in SEQ ID NO 2379: from 44 to 83
 - Alignment No. 14920
 - gi No. 4185138

- % Identity 81
- Alignment Length 42
- Location of Alignment in SEQ ID NO 2379: from 42 to 83
- Alignment No. 14921
- gi No. 4503507
- % Identity 75
- Alignment Length 40
- Location of Alignment in SEQ ID NO 2379: from 44 to 83
- (B) Polypeptide Sequence
 - Pat. Appln. SEQ ID NO 2380
 - Ceres seq_id 1503277
 - Location of start within SEQ ID NO 2378: at 115 nt.
- (C) Nomination and Annotation of Domains within Predicted Polypeptide(s)
 - (D) Related Amino Acid Sequences
 - Alignment No. 14922
 - qi No. 1174492
 - % Identity 76.2
 - Alignment Length 42
 - Location of Alignment in SEQ ID NO 2380: from 4 to 45
 - Alignment No. 14923
 - gi No. 2494300
 - % Identity 76.2
 - Alignment Length 42
 - Location of Alignment in SEQ ID NO 2380: from 4 to 45
 - Alignment No. 14924
 - gi No. 2832707
 - % Identity 81
 - Alignment Length 42
 - Location of Alignment in SEQ ID NO 2380: from 4 to 45
 - Alignment No. 14925
 - gi No. 3142294
 - % Identity 78.3
 - Alignment Length 46
 - Location of Alignment in SEQ ID NO 2380: from 1 to 45
 - Alignment No. 14926
 - gi No. 3790165
 - % Identity 72.5
 - Alignment Length 40
 - Location of Alignment in SEQ ID NO 2380: from 6 to 45
 - Alignment No. 14927
 - gi No. 3790184
 - % Identity 75
 - Alignment Length 40
 - Location of Alignment in SEQ ID NO 2380: from 6 to 45
 - Alignment No. 14928
 - gi No. 4185138
 - % Identity 81
 - Alignment Length 42
 - Location of Alignment in SEQ ID NO 2380: from 4 to 45
 - Alignment No. 14929

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- gi No. 4503507
- % Identity 75
- Alignment Length 40
- Location of Alignment in SEQ ID NO 2380: from 6 to 45
- (B) Polypeptide Sequence
 - Pat. Appln. SEQ ID NO 2381
 - Ceres seq id 1503278
 - Location of start within SEQ ID NO 2378: at 233 nt.
- - Alignment No. 14930
 - Elongation factor Tu family
 - Location within SEQ ID NO 2381: from 4 to 76 aa.
 - (D) Related Amino Acid Sequences
 - Alignment No. 14931
 - gi No. 1174492
 - % Identity 82.1
 - Alignment Length 39
 - Location of Alignment in SEQ ID NO 2381: from 4 to 42
 - Alignment No. 14932
 - gi No. 2494300
 - % Identity 76.6
 - Alignment Length 64
 - Location of Alignment in SEQ ID NO 2381: from 4 to 67
 - Alignment No. 14933
 - gi No. 2494301
 - % Identity 77.3
 - Alignment Length 66
 - Location of Alignment in SEQ ID NO 2381: from 4 to 69
 - Alignment No. 14934
 - gi No. 2832707
 - % Identity 89.2
 - Alignment Length 74
 - Location of Alignment in SEQ ID NO 2381: from 4 to 76
 - Alignment No. 14935
 - gi No. 3142294
 - % Identity 90.5
 - Alignment Length 74
 - Location of Alignment in SEQ ID NO 2381: from 4 to 76
 - Alignment No. 14936
 - gi No. 3790165
 - % Identity 70.7
 - Alignment Length 75
 - Location of Alignment in SEQ ID NO 2381: from 4 to 76
 - Alignment No. 14937
 - gi No. 3790184
 - % Identity 75
 - Alignment Length 68
 - Location of Alignment in SEQ ID NO 2381: from 4 to 71
 - Alignment No. 14938
 - gi No. 417179

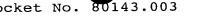
- % Identity 73.5
- Alignment Length 68
- Location of Alignment in SEQ ID NO 2381: from 4 to 71
- Alignment No. 14939
- gi No. 4185138
- % Identity 73
- Alignment Length 74
- Location of Alignment in SEQ ID NO 2381: from 4 to 76
- Alignment No. 14940
- gi No. 4503507
- % Identity 75
- Alignment Length 68
- Location of Alignment in SEQ ID NO 2381: from 4 to 71

- (A) Polynucleotide Sequence
 - Pat. Appln. SEQ ID NO 2382
 - Ceres seq id 1503279
 - (B) Polypeptide Sequence
 - Pat. Appln. SEQ ID NO 2383
 - Ceres seq_id 1503280
 - Location of start within SEQ ID NO 2382: at 3 nt.
- - (D) Related Amino Acid Sequences
 - Alignment No. 14941
 - gi No. 4512664
 - % Identity 93.3
 - Alignment Length 15
 - Location of Alignment in SEQ ID NO 2383: from 1 to 15
 - Alignment No. 14942
 - gi No. 4874278
 - % Identity 93.3
 - Alignment Length 15
 - Location of Alignment in SEQ ID NO 2383: from 1 to 15
 - Alignment No. 14943
 - gi No. 4902470
 - % Identity 93.3
 - Alignment Length 15
 - Location of Alignment in SEQ ID NO 2383: from 1 to 15 $\,$
 - Alignment No. 14944
 - gi No. 4902877
 - % Identity 93.3
 - Alignment Length 15
 - Location of Alignment in SEQ ID NO 2383: from 1 to 15
 - Alignment No. 14945
 - gi No. 4902879
 - % Identity 93.3
 - Alignment Length 15
 - Location of Alignment in SEQ ID NO 2383: from 1 to 15
 - (B) Polypeptide Sequence
 - Pat. Appln. SEQ ID NO 2384
 - Ceres seq_id 1503281

- Location of start within SEQ ID NO 2382: at 98 nt.
- - (D) Related Amino Acid Sequences
 - (B) Polypeptide Sequence
 - Pat. Appln. SEQ ID NO 2385
 - Ceres seq id 1503282
 - Location of start within SEQ ID NO 2382: at 133 nt.
- (C) Nomination and Annotation of Domains within Predicted Polypeptide(s)
 - (D) Related Amino Acid Sequences
 - Alignment No. 14946
 - gi No. 4512664
 - % Identity 70.6
 - Alignment Length 85
 - Location of Alignment in SEQ ID NO 2385: from 1 to 49

- (A) Polynucleotide Sequence
 - Pat. Appln. SEQ ID NO 2386
 - Ceres seq_id 1503297
 - (B) Polypept \overline{i} de Sequence
 - Pat. Appln. SEQ ID NO 2387
 - Ceres seq_id 1503298
 - Location of start within SEQ ID NO 2386: at 3 nt.
- - Alignment No. 14947
 - C2 domain
 - Location within SEQ ID NO 2387: from 27 to 84 aa.
 - (D) Related Amino Acid Sequences

- (A) Polynucleotide Sequence
 - Pat. Appln. SEQ ID NO 2388
 - Ceres seq_id 1503299
 - (B) Polypeptide Sequence
 - Pat. Appln. SEQ ID NO 2389
 - Ceres seq_id 1503300
 - Location of start within SEQ ID NO 2388: at 3 nt.
- (C) Nomination and Annotation of Domains within Predicted Polypeptide(s) $\label{eq:condition}$
 - Alignment No. 14948
 - Eukaryotic protein kinase domain
 - Location within SEQ ID NO 2389: from 1 to 54 aa.
 - (D) Related Amino Acid Sequences
 - Alignment No. 14949
 - qi No. 2191149
 - % Identity 74
 - Alignment Length 50
 - Location of Alignment in SEQ ID NO 2389: from 1 to 50
 - Alignment No. 14950
 - gi No. 2505874



- % Identity 74
- Alignment Length 50
- Location of Alignment in SEQ ID NO 2389: from 1 to 50
- Alignment No. 14951
- qi No. 3482919
- % Identity 70.4
- Alignment Length 54
- Location of Alignment in SEQ ID NO 2389: from 1 to 54
- Alignment No. 14952
- gi No. 4204849
- % Identity 70
- Alignment Length 50
- Location of Alignment in SEQ ID NO 2389: from 1 to 50
- Alignment No. 14953
- qi No. 4263791
- % Identity 74.7
- Alignment Length 79
- Location of Alignment in SEQ ID NO 2389: from 1 to 79
- Alignment No. 14954
- gi No. 4512659
- % Identity 70.4
- Alignment Length 54
- Location of Alignment in SEQ ID NO 2389: from 1 to 54
- Alignment No. 14955
- gi No. 4836880
- % Identity 71.4
- Alignment Length 56
- Location of Alignment in SEQ ID NO 2389: from 1 to 56
- Alignment No. 14956
- gi No. 5042449
- % Identity 75
- Alignment Length 56
- Location of Alignment in SEQ ID NO 2389: from 1 to 56

- (A) Polynucleotide Sequence
 - Pat. Appln. SEQ ID NO 2390
 - Ceres seq id 1503305
 - (B) Polypeptide Sequence
 - Pat. Appln. SEQ ID NO 2391
 - Ceres seq_id 1503306
 - Location of start within SEQ ID NO 2390: at 2 nt.
- (C) Nomination and Annotation of Domains within Predicted Polypeptide(s)
 - (D) Related Amino Acid Sequences
 - (B) Polypeptide Sequence
 - Pat. Appln. SEQ ID NO 2392
 - Ceres seq id 1503307
 - Location of start within SEQ ID NO 2390: at 3 nt.
- (C) Nomination and Annotation of Domains within Predicted Polypeptide(s)
 - Alignment No. 14957

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- Major intrinsic protein
- Location within SEQ ID NO 2392: from 35 to 135 aa.
- (D) Related Amino Acid Sequences
 - Alignment No. 14958
 - gi No. 1076687
 - % Identity 80.2
 - Alignment Length 106
 - Location of Alignment in SEQ ID NO 2392: from 30 to 135
 - Alignment No. 14959
 - gi No. 1212915
 - % Identity 71.7
 - Alignment Length 113
 - Location of Alignment in SEQ ID NO 2392: from 25 to 137
 - Alignment No. 14960
 - gi No. 1212921
 - % Identity 75.2
 - Alignment Length 113
 - Location of Alignment in SEQ ID NO 2392: from 25 to 137
 - Alignment No. 14961
 - gi No. 1212923
 - % Identity 72.6
 - Alignment Length 113
 - Location of Alignment in SEQ ID NO 2392: from 25 to 137
 - Alignment No. 14962
 - gi No. 126959
 - % Identity 77.5
 - Alignment Length 111
 - Location of Alignment in SEQ ID NO 2392: from 25 to 135
 - Alignment No. 14963
 - gi No. 1518057
 - % Identity 78.4
 - Alignment Length 111
 - Location of Alignment in SEQ ID NO 2392: from 25 to 135
 - Alignment No. 14964
 - gi No. 1743369
 - % Identity 74.8
 - Alignment Length 111
 - Location of Alignment in SEQ ID NO 2392: from 25 to 135
 - Alignment No. 14965
 - gi No. 1794147
 - % Identity 76.6
 - Alignment Length 111
 - Location of Alignment in SEQ ID NO 2392: from 25 to 135
 - Alignment No. 14966
 - gi No. 2058706
 - % Identity 80.2
 - Alignment Length 111
 - Location of Alignment in SEQ ID NO 2392: from 25 to 135
 - Alignment No. 14967
 - gi No. 2245093
 - % Identity 74.3

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- Alignment Length 113
- Location of Alignment in SEQ ID NO 2392: from 25 to 137
- Alignment No. 14968
- gi No. 257238
- % Identity 73
- Alignment Length 111
- Location of Alignment in SEQ ID NO 2392: from 25 to 135
- Alignment No. 14969
- gi No. 267135
- % Identity 77.5
- Alignment Length 111
- Location of Alignment in SEQ ID NO 2392: from 25 to 135
- Alignment No. 14970
- gi No. 3264596
- % Identity 80.2
- Alignment Length 111
- Location of Alignment in SEQ ID NO 2392: from 25 to 135
- Alignment No. 14971
- gi No. 3298458
- % Identity 71.4
- Alignment Length 35
- Location of Alignment in SEQ ID NO 2392: from 103 to 137
- Alignment No. 14972
- gi No. 461929
- % Identity 80.2
- Alignment Length 111
- Location of Alignment in SEQ ID NO 2392: from 25 to 135 $\,$
- Alignment No. 14973
- gi No. 4884870
- % Identity 75.4
- Alignment Length 69
- Location of Alignment in SEQ ID NO 2392: from 69 to 137
- (B) Polypeptide Sequence
 - Pat. Appln. SEQ ID NO 2393
 - Ceres seq_id 1503308
 - Location of start within SEQ ID NO 2390: at 75 nt.
- (C) Nomination and Annotation of Domains within Predicted Polypeptide(s) $% \left(\frac{1}{2}\right) =\frac{1}{2}\left(\frac{1}{2}\right) +\frac{1}{2}\left(\frac{1}{2}\right) +\frac{$
 - Alignment No. 14974
 - Major intrinsic protein
 - Location within SEQ ID NO 2393: from 11 to 111 aa.
 - (D) Related Amino Acid Sequences
 - Alignment No. 14975
 - gi No. 1076687
 - % Identity 80.2
 - Alignment Length 106
 - Location of Alignment in SEQ ID NO 2393: from 6 to 111
 - Alignment No. 14976
 - gi No. 1212915
 - % Identity 71.7
 - Alignment Length 113

- Location of Alignment in SEQ ID NO 2393: from 1 to 113
- Alignment No. 14977
- gi No. 1212921
- % Identity 75.2
- Alignment Length 113
- Location of Alignment in SEQ ID NO 2393: from 1 to 113
- Alignment No. 14978
- gi No. 1212923
- % Identity 72.6
- Alignment Length 113
- Location of Alignment in SEQ ID NO 2393: from 1 to 113
- Alignment No. 14979
- gi No. 126959
- % Identity 77.5
- Alignment Length 111
- Location of Alignment in SEQ ID NO 2393: from 1 to 111
- Alignment No. 14980
- gi No. 1518057
- % Identity 78.4
- Alignment Length 111
- Location of Alignment in SEQ ID NO 2393: from 1 to 111
- Alignment No. 14981
- gi No. 1743369
- % Identity 74.8
- Alignment Length 111
- Location of Alignment in SEQ ID NO 2393: from 1 to 111
- Alignment No. 14982
- gi No. 1794147
- % Identity 76.6
- Alignment Length 111
- Location of Alignment in SEQ ID NO 2393: from 1 to 111
- Alignment No. 14983
- gi No. 2058706
- % Identity 80.2
- Alignment Length 111
- Location of Alignment in SEQ ID NO 2393: from 1 to 111
- Alignment No. 14984
- gi No. 2245093
- % Identity 74.3
- Alignment Length 113
- Location of Alignment in SEQ ID NO 2393: from 1 to 113
- Alignment No. 14985
- gi No. 257238
- % Identity 73
- Alignment Length 111
- Location of Alignment in SEQ ID NO 2393: from 1 to 111
- Alignment No. 14986
- gi No. 267135
- % Identity 77.5
- Alignment Length 111
- Location of Alignment in SEQ ID NO 2393: from 1 to 111

- Alignment No. 14987
- gi No. 3264596
- % Identity 80.2
- Alignment Length 111
- Location of Alignment in SEQ ID NO 2393: from 1 to 111
- Alignment No. 14988
- gi No. 3298458
- % Identity 71.4
- Alignment Length 35
- Location of Alignment in SEQ ID NO 2393: from 79 to 113
- Alignment No. 14989
- gi No. 461929
- % Identity 80.2
- Alignment Length 111
- Location of Alignment in SEQ ID NO 2393: from 1 to 111
- Alignment No. 14990
- gi No. 4884870
- % Identity 75.4
- Alignment Length 69
- Location of Alignment in SEQ ID NO 2393: from 45 to 113

- (A) Polynucleotide Sequence
 - Pat. Appln. SEQ ID NO 2394
 - Ceres seq_id 1503322
 - (B) Polypeptide Sequence
 - Pat. Appln. SEQ ID NO 2395
 - Ceres seq_id 1503323
 - Location of start within SEQ ID NO 2394: at 2 nt.
- (C) Nomination and Annotation of Domains within Predicted Polypeptide(s) $% \left(\frac{1}{2}\right) =\frac{1}{2}\left(\frac{1}{2}\right) +\frac{1}{2}\left(\frac{1}{2}\right) +\frac{$
 - (D) Related Amino Acid Sequences
 - (B) Polypeptide Sequence
 - Pat. Appln. SEQ ID NO 2396
 - Ceres seq_id 1503324
 - Location of start within SEQ ID NO 2394: at 156 nt.
- (C) Nomination and Annotation of Domains within Predicted Polypeptide(s) $% \left(\frac{1}{2}\right) =\frac{1}{2}\left(\frac{1}{2}\right) +\frac{1}{2}\left(\frac{1}{2}\right) +\frac{$
 - Alignment No. 14991
 - short chain dehydrogenase
 - Location within SEQ ID NO 2396: from 7 to 102 aa.
 - (D) Related Amino Acid Sequences
 - (B) Polypeptide Sequence
 - Pat. Appln. SEQ ID NO 2397
 - Ceres seq id 1503325
 - Location of start within SEQ ID NO 2394: at 174 nt.
- - Alignment No. 14992
 - short chain dehydrogenase
 - Location within SEQ ID NO 2397: from 1 to 96 aa.

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(D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 314019 (A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 2398
- Ceres seq id 1503330
- (B) Polypeptide Sequence
 - Pat. Appln. SEQ ID NO 2399
 - Ceres seq_id 1503331
 - Location of start within SEQ ID NO 2398: at 42 nt.
- (C) Nomination and Annotation of Domains within Predicted Polypeptide(s) $% \left(\frac{1}{2}\right) =\frac{1}{2}\left(\frac{1}{2}\right) +\frac{1}{2}\left(\frac{1}{2}\right) +\frac{$
 - (D) Related Amino Acid Sequences
 - Alignment No. 14993
 - gi No. 4680192
 - % Identity 87.4
 - Alignment Length 143
 - Location of Alignment in SEQ ID NO 2399: from 6 to 148

- (A) Polynucleotide Sequence
 - Pat. Appln. SEQ ID NO 2400
 - Ceres seq_id 1503332
 - (B) Polypeptide Sequence
 - Pat. Appln. SEQ ID NO 2401
 - Ceres seq_id 1503333
 - Location of start within SEQ ID NO 2400: at 132 nt.
- (C) Nomination and Annotation of Domains within Predicted Polypeptide(s)
 - (D) Related Amino Acid Sequences
 - Alignment No. 14994
 - gi No. 2997589
 - % Identity 98.2
 - Alignment Length 109
 - Location of Alignment in SEQ ID NO 2401: from 1 to 105
 - Alignment No. 14995
 - gi No. 2997591
 - % Identity 84.3
 - Alignment Length 108
 - Location of Alignment in SEQ ID NO 2401: from 1 to 105
 - Alignment No. 14996
 - gi No. 2997593
 - % Identity 77.8
 - Alignment Length 108
 - Location of Alignment in SEQ ID NO 2401: from 1 to 105
 - Alignment No. 14997
 - gi No. 3367515
 - % Identity 86.1
 - Alignment Length 108
 - Location of Alignment in SEQ ID NO 2401: from 1 to 105
 - (B) Polypeptide Sequence
 - Pat. Appln. SEQ ID NO 2402
 - Ceres seq id 1503334
 - Location of start within SEQ ID NO 2400: at 156 nt.

- - (D) Related Amino Acid Sequences
 - Alignment No. 14998
 - gi No. 2997589
 - % Identity 98.2
 - Alignment Length 109
 - Location of Alignment in SEQ ID NO 2402: from 1 to 97
 - Alignment No. 14999
 - gi No. 2997591
 - % Identity 84.3
 - Alignment Length 108
 - Location of Alignment in SEQ ID NO 2402: from 1 to 97
 - Alignment No. 15000
 - gi No. 2997593
 - % Identity 77.8
 - Alignment Length 108
 - Location of Alignment in SEQ ID NO 2402: from 1 to 97
 - Alignment No. 15001
 - gi No. 3367515
 - % Identity 86.1
 - Alignment Length 108
 - Location of Alignment in SEQ ID NO 2402: from 1 to 97
 - (B) Polypeptide Sequence
 - Pat. Appln. SEQ ID NO 2403
 - Ceres seq_id 1503335
 - Location of start within SEQ ID NO 2400: at 183 nt.
- (C) Nomination and Annotation of Domains within Predicted Polypeptide(s)
 - (D) Related Amino Acid Sequences
 - Alignment No. 15002
 - gi No. 2997589
 - % Identity 98.2
 - Alignment Length 109
 - Location of Alignment in SEQ ID NO 2403: from 1 to 88
 - Alignment No. 15003
 - gi No. 2997591
 - % Identity 84.3
 - Alignment Length 108
 - Location of Alignment in SEQ ID NO 2403: from 1 to 88
 - Alignment No. 15004
 - gi No. 2997593
 - % Identity 77.8
 - Alignment Length 108
 - Location of Alignment in SEQ ID NO 2403: from 1 to 88
 - Alignment No. 15005
 - gi No. 3367515
 - % Identity 86.1
 - Alignment Length 108
 - Location of Alignment in SEQ ID NO 2403: from 1 to 88

- (A) Polynucleotide Sequence
 - Pat. Appln. SEQ ID NO 2404
 - Ceres seq_id 1503336
 - (B) Polypeptide Sequence
 - Pat. Appln. SEQ ID NO 2405
 - Ceres seq_id 1503337
 - Location of start within SEQ ID NO 2404: at 133 nt.
- - (D) Related Amino Acid Sequences
 - Alignment No. 15006
 - gi No. 4006906
 - % Identity 75
 - Alignment Length 12
 - Location of Alignment in SEQ ID NO 2405: from 2 to 13

- (A) Polynucleotide Sequence
 - Pat. Appln. SEQ ID NO 2406
 - Ceres seq_id 1503342
 - (B) Polypeptide Sequence
 - Pat. Appln. SEQ ID NO 2407
 - Ceres seq_id 1503343
 - Location of start within SEQ ID NO 2406: at 2 nt.
- (C) Nomination and Annotation of Domains within Predicted Polypeptide(s)
 - (D) Related Amino Acid Sequences
 - Alignment No. 15007
 - gi No. 3786009
 - % Identity 87.3
 - Alignment Length 157
 - Location of Alignment in SEQ ID NO 2407: from 1 to 157
 - (B) Polypeptide Sequence
 - Pat. Appln. SEQ ID NO 2408
 - Ceres seq_id 1503344
 - Location of start within SEQ ID NO 2406: at 179 nt.
- - (D) Related Amino Acid Sequences
 - Alignment No. 15008
 - gi No. 3786009
 - % Identity 87.3
 - Alignment Length 157
 - Location of Alignment in SEQ ID NO 2408: from 1 to 98

- (A) Polynucleotide Sequence
 - Pat. Appln. SEQ ID NO 2409
 - Ceres seq_id 1503345
 - (B) Polypeptide Sequence
 - Pat. Appln. SEQ ID NO 2410
 - Ceres seq_id 1503346
 - Location of start within SEQ ID NO 2409: at 2 nt.
- (C) Nomination and Annotation of Domains within Predicted Polypeptide(s)
 - (D) Related Amino Acid Sequences

- (B) Polypeptide Sequence
 - Pat. Appln. SEQ ID NO 2411
 - Ceres seq id 1503347
 - Location of start within SEQ ID NO 2409: at 39 nt.
- (C) Nomination and Annotation of Domains within Predicted Polypeptide(s)
 - (D) Related Amino Acid Sequences
 - Alignment No. 15009
 - gi No. 2150000
 - % Identity 71.7
 - Alignment Length 53
 - Location of Alignment in SEQ ID NO 2411: from 1 to 53

- (A) Polynucleotide Sequence
 - Pat. Appln. SEQ ID NO 2412
 - Ceres seq_id 1503351
 - (B) Polypeptide Sequence
 - Pat. Appln. SEQ ID NO 2413
 - Ceres seq_id 1503352
 - Location of start within SEQ ID NO 2412: at 1 nt.
- - (D) Related Amino Acid Sequences
 - Alignment No. 15010
 - gi No. 1185397
 - % Identity 72.7
 - Alignment Length 11
 - Location of Alignment in SEQ ID NO 2413: from 14 to 24
 - Alignment No. 15011
 - gi No. 1644455
 - % Identity 81.8
 - Alignment Length 11
 - Location of Alignment in SEQ ID NO 2413: from 14 to 24
 - Alignment No. 15012
 - gi No. 1644455
 - % Identity 72.7
 - Alignment Length 11
 - Location of Alignment in SEQ ID NO 2413: from 14 to 24
 - Alignment No. 15013
 - gi No. 1644457
 - % Identity 81.8
 - Alignment Length 11
 - Location of Alignment in SEQ ID NO 2413: from 14 to 24
 - Alignment No. 15014
 - gi No. 1644457
 - % Identity 72.7
 - Alignment Length 11
 - Location of Alignment in SEQ ID NO 2413: from 14 to 24
 - Alignment No. 15015
 - gi No. 1644457
 - % Identity 72.7
 - Alignment Length 11

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- Location of Alignment in SEQ ID NO 2413: from 14 to 24
- Alignment No. 15016
- gi No. 1644457
- % Identity 72.7
- Alignment Length 11
- Location of Alignment in SEQ ID NO 2413: from 14 to 24
- Alignment No. 15017
- gi No. 1644459
- % Identity 81.8
- Alignment Length 11
- Location of Alignment in SEQ ID NO 2413: from 14 to 24
- Alignment No. 15018
- gi No. 1644459
- % Identity 72.7
- Alignment Length 11
- Location of Alignment in SEQ ID NO 2413: from 14 to 24
- Alignment No. 15019
- gi No. 1644459
- % Identity 72.7
- Alignment Length 11
- Location of Alignment in SEQ ID NO 2413: from 14 to 24
- Alignment No. 15020
- qi No. 1644459
- % Identity 72.7
- Alignment Length 11
- Location of Alignment in SEQ ID NO 2413: from 14 to 24
- Alignment No. 15021
- gi No. 1644461
- % Identity 81.8
- Alignment Length 11
- Location of Alignment in SEQ ID NO 2413: from 14 to 24 $\,$
- Alignment No. 15022
- gi No. 1644461
- % Identity 72.7
- Alignment Length 11
- Location of Alignment in SEQ ID NO 2413: from 14 to 24
- Alignment No. 15023
- gi No. 1644461
- % Identity 72.7
- Alignment Length 11
- Location of Alignment in SEQ ID NO 2413: from 14 to 24
- Alignment No. 15024
- gi No. 1644461
- % Identity 72.7
- Alignment Length 11
- Location of Alignment in SEQ ID NO 2413: from 14 to 24
- Alignment No. 15025
- gi No. 178014
- % Identity 75
- Alignment Length 13
- Location of Alignment in SEQ ID NO 2413: from 13 to 24

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- Alignment No. 15026
 - gi No. 1914853
 - % Identity 72.7
 - Alignment Length 11
 - Location of Alignment in SEQ ID NO 2413: from 14 to 24
 - Alignment No. 15027
 - gi No. 19923
 - % Identity 72.7
 - Alignment Length 11
 - Location of Alignment in SEQ ID NO 2413: from 14 to 24
- Alignment No. 15028
 - gi No. 2244878
- % Identity 72.7
- Alignment Length 11
- Location of Alignment in SEQ ID NO 2413: from 14 to 24
- Alignment No. 15029
- gi No. 2462823
- % Identity 72.7
- Alignment Length 11
- Location of Alignment in SEQ ID NO 2413: from 14 to 24
- Alignment No. 15030
- gi No. 322755
- % Identity 72.7
- Alignment Length 11
- Location of Alignment in SEQ ID NO 2413: from 15 to 25
- Alignment No. 15031
- gi No. 322755
- % Identity 72.7
- Alignment Length 11
- Location of Alignment in SEQ ID NO 2413: from 15 to 25
- Alignment No. 15032
- gi No. 322755
- % Identity 71.4
- Alignment Length 14
- Location of Alignment in SEQ ID NO 2413: from 14 to 27
- Alignment No. 15033
- gi No. 322757
- % Identity 72.7
- Alignment Length 11
- Location of Alignment in SEQ ID NO 2413: from 14 to 24
- Alignment No. 15034
- gi No. 3551531
- % Identity 81.8
- Alignment Length 11
- Location of Alignment in SEQ ID NO 2413: from 14 to 24
- Alignment No. 15035
- gi No. 5306259
- % Identity 72.7
- Alignment Length 11
- Location of Alignment in SEQ ID NO 2413: from 14 to 24
```

- (B) Polypeptide Sequence
 - Pat. Appln. SEQ ID NO 2414
 - Ceres seq_id 1503353
 - Location of start within SEQ ID NO 2412: at 3 nt.
- (C) Nomination and Annotation of Domains within Predicted Polypeptide(s)
 - (D) Related Amino Acid Sequences

- (A) Polynucleotide Sequence
 - Pat. Appln. SEQ ID NO 2415
 - Ceres seq_id 1503354
 - (B) Polypeptide Sequence
 - Pat. Appln. SEQ ID NO 2416
 - Ceres seq_id 1503355
 - Location of start within SEQ ID NO 2415: at 3 nt.
- - (D) Related Amino Acid Sequences
 - (B) Polypeptide Sequence
 - Pat. Appln. SEQ ID NO 2417
 - Ceres seq_id 1503356
 - Location of start within SEQ ID NO 2415: at 9 nt.
- - (D) Related Amino Acid Sequences
 - (B) Polypeptide Sequence
 - Pat. Appln. SEQ ID NO 2418
 - Ceres seq_id 1503357
 - Location of start within SEQ ID NO 2415: at 103 nt.
- (C) Nomination and Annotation of Domains within Predicted Polypeptide(s) $\label{eq:polypeptide} % \begin{array}{c} (C) & (C)$
 - Alignment No. 15036
 - DnaJ domain
 - Location within SEQ ID NO 2418: from 24 to 75 aa.
 - (D) Related Amino Acid Sequences

- (A) Polynucleotide Sequence
 - Pat. Appln. SEQ ID NO 2419
 - Ceres seq_id 1503378
 - (B) Polypeptide Sequence
 - Pat. Appln. SEQ ID NO 2420
 - Ceres seq_id 1503379
 - Location of start within SEQ ID NO 2419: at 2 nt.
- (C) Nomination and Annotation of Domains within Predicted Polypeptide(s) $% \left(\frac{1}{2}\right) =\frac{1}{2}\left(\frac{1}{2}\right) +\frac{1}{2}\left(\frac{1}{2}\right) +\frac{$
 - Alignment No. 15037
 - Protein phosphatase 2C
 - Location within SEQ ID NO 2420: from 3 to 84 aa.
 - (D) Related Amino Acid Sequences

- (A) Polynucleotide Sequence
 - Pat. Appln. SEQ ID NO 2421
 - Ceres seq id 1503400
 - (B) Polypeptide Sequence
 - Pat. Appln. SEQ ID NO 2422
 - Ceres seq id 1503401
 - Location of start within SEQ ID NO 2421: at 2 nt.
- (C) Nomination and Annotation of Domains within Predicted Polypeptide(s)
 - (D) Related Amino Acid Sequences
 - Alignment No. 15038
 - gi No. 445612
 - % Identity 72.1
 - Alignment Length 43
 - Location of Alignment in SEQ ID NO 2422: from 39 to 81
 - (B) Polypeptide Sequence
 - Pat. Appln. SEQ ID NO 2423
 - Ceres seq_id 1503402
 - Location of start within SEQ ID NO 2421: at 3 nt.
- (C) Nomination and Annotation of Domains within Predicted Polypeptide(s)
 - (D) Related Amino Acid Sequences
 - (B) Polypeptide Sequence
 - Pat. Appln. SEQ ID NO 2424
 - Ceres seq id 1503403
 - Location of start within SEQ ID NO 2421: at 101 nt.
- (C) Nomination and Annotation of Domains within Predicted Polypeptide(s)
 - (D) Related Amino Acid Sequences
 - Alignment No. 15039
 - gi No. 445612
 - % Identity 72.1
 - Alignment Length 43
 - Location of Alignment in SEQ ID NO 2424: from 6 to 48

- (A) Polynucleotide Sequence
 - Pat. Appln. SEQ ID NO 2425
 - Ceres seq_id 1503422
 - (B) Polypeptide Sequence
 - Pat. Appln. SEQ ID NO 2426
 - Ceres seq_id 1503423
 - Location of start within SEQ ID NO 2425: at 1 nt.
- (C) Nomination and Annotation of Domains within Predicted Polypeptide(s)
 - (D) Related Amino Acid Sequences
 - Alignment No. 15040
 - gi No. 1743388
 - % Identity 94.2
 - Alignment Length 86
 - Location of Alignment in SEQ ID NO 2426: from 77 to 161
 - (B) Polypeptide Sequence
 - Pat. Appln. SEQ ID NO 2427

Tab:

- Ceres seg id 1503424
- Location of start within SEQ ID NO 2425: at 133 nt.
- (C) Nomination and Annotation of Domains within Predicted Polypeptide(s)
 - (D) Related Amino Acid Sequences
 - Alignment No. 15041
 - gi No. 1743388
 - % Identity 94.2
 - Alignment Length 86
 - Location of Alignment in SEQ ID NO 2427: from 33 to 117

Maximum Length Sequence corresponding to clone ID 314420

- (A) Polynucleotide Sequence
 - Pat. Appln. SEQ ID NO 2428
 - Ceres seq_id 1503429
 - (B) Polypeptide Sequence
 - Pat. Appln. SEQ ID NO 2429
 - Ceres seq_id 1503430
 - Location of start within SEQ ID NO 2428: at 3 nt.
- (C) Nomination and Annotation of Domains within Predicted Polypeptide(s) $\label{eq:continuous}$
 - (D) Related Amino Acid Sequences
 - Alignment No. 15042
 - gi No. 2914700
 - % Identity 86.7
 - Alignment Length 30
 - Location of Alignment in SEQ ID NO 2429: from 2 to 31
 - (B) Polypeptide Sequence
 - Pat. Appln. SEQ ID NO 2430
 - Ceres seq_id 1503431
 - Location of start within SEQ ID NO 2428: at 183 nt.
- - (D) Related Amino Acid Sequences
 - (B) Polypeptide Sequence
 - Pat. Appln. SEQ ID NO 2431
 - Ceres seq_id 1503432
 - Location of start within SEQ ID NO 2428: at 269 nt.
- - (D) Related Amino Acid Sequences

- (A) Polynucleotide Sequence
 - Pat. Appln. SEQ ID NO 2432
 - Ceres seq_id 1503443
 - (B) Polypeptide Sequence
 - Pat. Appln. SEQ ID NO 2433
 - Ceres seq_id 1503444
 - Location of start within SEQ ID NO 2432: at 1 nt.
- - (D) Related Amino Acid Sequences

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- (B) Polypeptide Sequence
 - Pat. Appln. SEQ ID NO 2434 Ceres seq_id 1503445

 - Location of start within SEQ ID NO 2432: at 2 nt.
- (C) Nomination and Annotation of Domains within Predicted Polypeptide(s)
 - (D) Related Amino Acid Sequences
 - Alignment No. 15043
 - gi No. 119111
 - % Identity 78.6
 - Alignment Length 14
 - Location of Alignment in SEQ ID NO 2434: from 38 to 51
 - Alignment No. 15044
 - gi No. 4008584
 - % Identity 75
 - Alignment Length 12
 - Location of Alignment in SEQ ID NO 2434: from 41 to 51
 - Alignment No. 15045
 - gi No. 4008584
 - % Identity 73.3
 - Alignment Length 15
 - Location of Alignment in SEQ ID NO 2434: from 37 to 51
 - Alignment No. 15046
 - gi No. 628112
 - % Identity 78.6
 - Alignment Length 14
 - Location of Alignment in SEQ ID NO 2434: from 38 to 51
 - Alignment No. 15047
 - gi No. 628185
 - % Identity 78.6
 - Alignment Length 14
 - Location of Alignment in SEQ ID NO 2434: from 38 to 51
 - Alignment No. 15048
 - gi No. 688080
 - % Identity 75
 - Alignment Length 12
 - Location of Alignment in SEQ ID NO 2434: from 42 to 52
 - (B) Polypeptide Sequence
 - Pat. Appln. SEQ ID NO 2435
 - Ceres seq_id 1503446
 - Location of start within SEQ ID NO 2432: at 101 nt.
- (C) Nomination and Annotation of Domains within Predicted Polypeptide(s)
 - (D) Related Amino Acid Sequences
 - Alignment No. 15049
 - gi No. 119111
 - % Identity 78.6
 - Alignment Length 14
 - Location of Alignment in SEQ ID NO 2435: from 5 to 18
 - Alignment No. 15050
 - gi No. 4008584
 - % Identity 75

- Alignment Length 12
- Location of Alignment in SEQ ID NO 2435: from 8 to 18
- Alignment No. 15051
- gi No. 4008584
- % Identity 73.3
- Alignment Length 15
- Location of Alignment in SEQ ID NO 2435: from 4 to 18
- Alignment No. 15052
- gi No. 628112
- % Identity 78.6
- Alignment Length 14
- Location of Alignment in SEQ ID NO 2435: from 5 to 18
- Alignment No. 15053
- gi No. 628185
- % Identity 78.6
- Alignment Length 14
- Location of Alignment in SEQ ID NO 2435: from 5 to 18
- Alignment No. 15054
- gi No. 688080
- % Identity 75
- Alignment Length 12
- Location of Alignment in SEQ ID NO 2435: from 9 to 19

- (A) Polynucleotide Sequence
 - Pat. Appln. SEQ ID NO 2436
 - Ceres seq_id 1503476
 - (B) Polypeptide Sequence
 - Pat. Appln. SEQ ID NO 2437
 - Ceres seq_id 1503477
 - Location of start within SEQ ID NO 2436: at 2 nt.
- - (D) Related Amino Acid Sequences
 - (B) Polypeptide Sequence
 - Pat. Appln. SEQ ID NO 2438
 - Ceres seq_id 1503478
 - Location of start within SEQ ID NO 2436: at 3 nt.
- - Alignment No. 15055
 - Chitin recognition protein
 - Location within SEQ ID NO 2438: from 44 to 77 aa.
 - Alignment No. 15056
 - Chitinases class I
 - Location within SEQ ID NO 2438: from 90 to 146 aa.
 - (D) Related Amino Acid Sequences
 - Alignment No. 15057
 - gi No. 299189
 - % Identity 71.4
 - Alignment Length 21
 - Location of Alignment in SEQ ID NO 2438: from 49 to 69

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- Alignment No. 15058
- gi No. 299190
- % Identity 71.4
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2438: from 49 to 69
- Alignment No. 15059
- gi No. 994881
- % Identity 75.8
- Alignment Length 33
- Location of Alignment in SEQ ID NO 2438: from 112 to 144
- (B) Polypeptide Sequence
 - Pat. Appln. SEQ ID NO 2439
 - Ceres seq_id 1503479
 - Location of start within SEQ ID NO 2436: at 60 nt.
- (C) Nomination and Annotation of Domains within Predicted Polypeptide(s)
 - Alignment No. 15060
 - Chitin recognition protein
 - Location within SEQ ID NO 2439: from 25 to 58 aa.
 - Alignment No. 15061
 - Chitinases class I
 - Location within SEQ ID NO 2439: from 71 to 127 aa.
 - (D) Related Amino Acid Sequences
 - Alignment No. 15062
 - gi No. 299189
 - % Identity 71.4
 - Alignment Length 21
 - Location of Alignment in SEQ ID NO 2439: from 30 to 50
 - Alignment No. 15063
 - gi No. 299190
 - % Identity 71.4
 - Alignment Length 21
 - Location of Alignment in SEQ ID NO 2439: from 30 to 50
 - Alignment No. 15064
 - qi No. 994881
 - % Identity 75.8
 - Alignment Length 33
 - Location of Alignment in SEQ ID NO 2439: from 93 to 125

- (A) Polynucleotide Sequence
 - Pat. Appln. SEQ ID NO 2440
 - Ceres seq_id 1503480
 - (B) Polypeptide Sequence
 - Pat. Appln. SEQ ID NO 2441
 - Ceres seq_id 1503481
 - Location of start within SEQ ID NO 2440: at 1 nt.
- (C) Nomination and Annotation of Domains within Predicted Polypeptide(s)
 - Alignment No. 15065
 - chorismate binding enzyme
 - Location within SEQ ID NO 2441: from 4 to 147 aa.

(D) Related Amino Acid Sequences - Alignment No. 15066 - gi No. 320552 - % Identity 82.6 - Alignment Length 144 - Location of Alignment in SEQ ID NO 2441: from 4 to 147 - Alignment No. 15067 - gi No. 320553 - % Identity 79.5 - Alignment Length 146 - Location of Alignment in SEQ ID NO 2441: from 2 to 147 - Alignment No. 15068 - gi No. 3348124 - % Identity 76.8 - Alignment Length 155 - Location of Alignment in SEQ ID NO 2441: from 2 to 155 - Alignment No. 15069 - gi No. 418133 - % Identity 82.6 - Alignment Length 144 - Location of Alignment in SEQ ID NO 2441: from 4 to 147 - Alignment No. 15070 - gi No. 418134 - % Identity 79.5 - Alignment Length 146 - Location of Alignment in SEQ ID NO 2441: from 2 to 147 - Alignment No. 15071 - gi No. 5360657 - % Identity 78.5 - Alignment Length 144 - Location of Alignment in SEQ ID NO 2441: from 4 to 147 - Alignment No. 15072 - gi No. 5360659 - % Identity 95.2 - Alignment Length 147 - Location of Alignment in SEQ ID NO 2441: from 1 to 147 - Alignment No. 15073 - gi No. 960289 - % Identity 83.3 - Alignment Length 144 - Location of Alignment in SEQ ID NO 2441: from 4 to 147 - Alignment No. 15074 - gi No. 960291 - % Identity 80.3 - Alignment Length 147 - Location of Alignment in SEQ ID NO 2441: from 1 to 147

- (B) Polypeptide Sequence
 - Pat. Appln. SEQ ID NO 2442
 - Ceres seq_id 1503482
 - Location of start within SEQ ID NO 2440: at 4 nt.

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- (C) Nomination and Annotation of Domains within Predicted Polypeptide(s) $% \left(\frac{1}{2}\right) =\frac{1}{2}\left(\frac{1}{2}\right) +\frac{1}{2}\left(\frac{1}{2}\right) +\frac{$
 - Alignment No. 15075
 - chorismate binding enzyme
 - Location within SEQ ID NO 2442: from 3 to 146 aa.
 - (D) Related Amino Acid Sequences
 - Alignment No. 15076
 - gi No. 320552
 - % Identity 82.6
 - Alignment Length 144
 - Location of Alignment in SEQ ID NO 2442: from 3 to 146
 - Alignment No. 15077
 - gi No. 320553
 - % Identity 79.5
 - Alignment Length 146
 - Location of Alignment in SEQ ID NO 2442: from 1 to 146
 - Alignment No. 15078
 - gi No. 3348124
 - % Identity 76.8
 - Alignment Length 155
 - Location of Alignment in SEQ ID NO 2442: from 1 to 154
 - Alignment No. 15079
 - gi No. 418133
 - % Identity 82.6
 - Alignment Length 144
 - Location of Alignment in SEQ ID NO 2442: from 3 to 146
 - Alignment No. 15080
 - gi No. 418134
 - % Identity 79.5
 - Alignment Length 146
 - Location of Alignment in SEQ ID NO 2442: from 1 to 146
 - Alignment No. 15081
 - gi No. 5360657
 - % Identity 78.5
 - Alignment Length 144
 - Location of Alignment in SEQ ID NO 2442: from 3 to 146
 - Alignment No. 15082
 - gi No. 5360659
 - % Identity 95.2
 - Alignment Length 147
 - Location of Alignment in SEQ ID NO 2442: from 1 to 146
 - Alignment No. 15083
 - gi No. 960289
 - % Identity 83.3
 - Alignment Length 144
 - Location of Alignment in SEQ ID NO 2442: from 3 to 146 $\,$
 - Alignment No. 15084
 - gi No. 960291
 - % Identity 80.3
 - Alignment Length 147
 - Location of Alignment in SEQ ID NO 2442: from 1 to 146

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- (B) Polypeptide Sequence
 - Pat. Appln. SEQ ID NO 2443
 - Ceres seq_id 1503483
 - Location of start within SEQ ID NO 2440: at 55 nt.
- - Alignment No. 15085
 - chorismate binding enzyme
 - Location within SEQ ID NO 2443: from 1 to 129 aa.
 - (D) Related Amino Acid Sequences
 - Alignment No. 15086
 - gi No. 320552
 - % Identity 82.6
 - Alignment Length 144
 - Location of Alignment in SEQ ID NO 2443: from 1 to 129
 - Alignment No. 15087
 - gi No. 320553
 - % Identity 79.5
 - Alignment Length 146
 - Location of Alignment in SEQ ID NO 2443: from 1 to 129
 - Alignment No. 15088
 - gi No. 3348124
 - % Identity 76.8
 - Alignment Length 155
 - Location of Alignment in SEQ ID NO 2443: from 1 to 137
 - Alignment No. 15089
 - gi No. 418133
 - % Identity 82.6
 - Alignment Length 144
 - Location of Alignment in SEQ ID NO 2443: from 1 to 129
 - Alignment No. 15090
 - gi No. 418134
 - % Identity 79.5
 - Alignment Length 146
 - Location of Alignment in SEQ ID NO 2443: from 1 to 129
 - Alignment No. 15091
 - gi No. 5360657
 - % Identity 78.5
 - Alignment Length 144
 - Location of Alignment in SEQ ID NO 2443: from 1 to 129
 - Alignment No. 15092
 - gi No. 5360659
 - % Identity 95.2
 - Alignment Length 147
 - Location of Alignment in SEQ ID NO 2443: from 1 to 129
 - Alignment No. 15093
 - gi No. 960289
 - % Identity 83.3
 - Alignment Length 144
 - Location of Alignment in SEQ ID NO 2443: from 1 to 129
 - Alignment No. 15094

- qi No. 960291
- % Identity 80.3
- Alignment Length 147
- Location of Alignment in SEQ ID NO 2443: from 1 to 129

- (A) Polynucleotide Sequence
 - Pat. Appln. SEQ ID NO 2444
 - Ceres seq_id 1503484
 - (B) Polypeptide Sequence
 - Pat. Appln. SEQ ID NO 2445
 - Ceres seq id 1503485
 - Location of start within SEQ ID NO 2444: at 1 nt.
- - Alignment No. 15095
 - Thioredoxin
 - Location within SEQ ID NO 2445: from 22 to 128 aa.
 - (D) Related Amino Acid Sequences
 - Alignment No. 15096
 - gi No. 3915131
 - % Identity 70.7
 - Alignment Length 123
 - Location of Alignment in SEQ ID NO 2445: from 16 to 138
 - (B) Polypeptide Sequence
 - Pat. Appln. SEQ ID NO 2446
 - Ceres seq_id 1503486
 - Location of start within SEQ ID NO 2444: at 46 nt.
- - Alignment No. 15097
 - Thioredoxin
 - Location within SEQ ID NO 2446: from 7 to 113 aa.
 - (D) Related Amino Acid Sequences
 - Alignment No. 15098
 - qi No. 3915131
 - % Identity 70.7
 - Alignment Length 123
 - Location of Alignment in SEQ ID NO 2446: from 1 to 123
 - (B) Polypeptide Sequence
 - Pat. Appln. SEQ ID NO 2447
 - Ceres seq_id 1503487
 - Location of start within SEQ ID NO 2444: at 109 nt.
- (C) Nomination and Annotation of Domains within Predicted Polypeptide(s) $\label{eq:polypeptide} % \begin{array}{c} (C) & (C)$
 - Alignment No. 15099
 - Thioredoxin
 - Location within SEQ ID NO 2447: from 1 to 92 aa.
 - (D) Related Amino Acid Sequences
 - Alignment No. 15100
 - gi No. 3915131
 - % Identity 70.7
 - Alignment Length 123

- Location of Alignment in SEQ ID NO 2447: from 1 to 102

Maximum Length Sequence corresponding to clone ID 314637

- (A) Polynucleotide Sequence
 - Pat. Appln. SEQ ID NO 2448
 - Ceres seq_id 1503492
 - (B) Polypeptide Sequence
 - Pat. Appln. SEQ ID NO 2449
 - Ceres seq id 1503493
 - Location of start within SEQ ID NO 2448: at 201 nt.
- (C) Nomination and Annotation of Domains within Predicted Polypeptide(s)
 - Alignment No. 15101
 - Chalcone and stilbene synthases
 - Location within SEQ ID NO 2449: from 12 to 62 aa.
 - (D) Related Amino Acid Sequences
 - Alignment No. 15102
 - gi No. 322636
 - % Identity 86.4
 - Alignment Length 22
 - Location of Alignment in SEQ ID NO 2449: from 41 to 62
 - (B) Polypeptide Sequence
 - Pat. Appln. SEQ ID NO 2450
 - Ceres seq_id 1503494
 - Location of start within SEQ ID NO 2448: at 228 nt.
- (C) Nomination and Annotation of Domains within Predicted Polypeptide(s)
 - Alignment No. 15103
 - Chalcone and stilbene synthases
 - Location within SEQ ID NO 2450: from 3 to 53 aa.
 - (D) Related Amino Acid Sequences
 - Alignment No. 15104
 - gi No. 322636
 - % Identity 86.4
 - Alignment Length 22
 - Location of Alignment in SEQ ID NO 2450: from 32 to 53
 - (B) Polypeptide Sequence
 - Pat. Appln. SEQ ID NO 2451
 - Ceres seq id 1503495
 - Location of start within SEQ ID NO 2448: at 261 nt.
- (C) Nomination and Annotation of Domains within Predicted Polypeptide(s)
 - (D) Related Amino Acid Sequences
 - Alignment No. 15105
 - gi No. 322636
 - % Identity 86.4
 - Alignment Length 22
 - Location of Alignment in SEQ ID NO 2451: from 21 to 42

- (A) Polynucleotide Sequence
 - Pat. Appln. SEQ ID NO 2452
 - Ceres seg id 1503496
 - (B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2453
- Ceres seq_id 1503497
- Location of start within SEQ ID NO 2452: at 1 nt.
- (C) Nomination and Annotation of Domains within Predicted Polypeptide(s)
 - Alignment No. 15106
 - 7 transmembrane receptor (rhodopsin family)
 - Location within SEQ ID NO 2453: from 9 to 136 aa.
 - Alignment No. 15107
 - 7 transmembrane receptor (rhodopsin family)
 - Location within SEQ ID NO 2453: from 28 to 151 aa.
 - Alignment No. 15108
 - Assemblin (Peptidase family S21)
 - Location within SEQ ID NO 2453: from 23 to 125 aa.
 - (D) Related Amino Acid Sequences
 - (B) Polypeptide Sequence
 - Pat. Appln. SEQ ID NO 2454
 - Ceres seq id 1503498
 - Location of start within SEQ ID NO 2452: at 1 nt.
- - Alignment No. 15109
 - 7 transmembrane receptor (rhodopsin family)
 - Location within SEQ ID NO 2454: from 9 to 136 aa.
 - Alignment No. 15110
 - 7 transmembrane receptor (rhodopsin family)
 - Location within SEQ ID NO 2454: from 28 to 151 aa.
 - Alignment No. 15111
 - Assemblin (Peptidase family S21)
 - Location within SEQ ID NO 2454: from 23 to 125 aa.
 - (D) Related Amino Acid Sequences
 - (B) Polypeptide Sequence
 - Pat. Appln. SEQ ID NO 2455
 - Ceres seq id 1503499
 - Location of start within SEQ ID NO 2452: at 3 nt.
- - (D) Related Amino Acid Sequences

- (A) Polynucleotide Sequence
 - Pat. Appln. SEQ ID NO 2456
 - Ceres seq id 1503507
 - (B) Polypeptide Sequence
 - Pat. Appln. SEQ ID NO 2457
 - Ceres seq_id 1503508
 - Location of start within SEQ ID NO 2456: at 3 nt.

- (D) Related Amino Acid Sequences
 - Alignment No. 15112
 - gi No. 2894378
 - % Identity 82.5
 - Alignment Length 114
 - Location of Alignment in SEQ ID NO 2457: from 1 to 114
- (B) Polypeptide Sequence
 - Pat. Appln. SEQ ID NO 2458
 - Ceres seq_id 1503509
 - Location of start within SEQ ID NO 2456: at 231 nt.
- (C) Nomination and Annotation of Domains within Predicted Polypeptide(s) $\label{eq:polypeptide} \begin{subarray}{ll} \end{subarray}$
 - (D) Related Amino Acid Sequences
 - Alignment No. 15113
 - qi No. 2894378
 - % Identity 82.5
 - Alignment Length 114
 - Location of Alignment in SEQ ID NO 2458: from 1 to 38

- (A) Polynucleotide Sequence
 - Pat. Appln. SEQ ID NO 2459
 - Ceres seq_id 1503510
 - (B) Polypeptide Sequence
 - Pat. Appln. SEQ ID NO 2460
 - Ceres seq id 1503511
 - Location of start within SEQ ID NO 2459: at 3 nt.
- (C) Nomination and Annotation of Domains within Predicted Polypeptide(s) $% \left(1\right) =\left(1\right) \left(1\right) +\left(1\right) \left(1\right) \left(1\right) +\left(1\right) \left(1\right)$
 - (D) Related Amino Acid Sequences
 - Alignment No. 15114
 - gi No. 4091080
 - % Identity 70.7
 - Alignment Length 59
 - Location of Alignment in SEQ ID NO 2460: from 1 to 57
 - (B) Polypeptide Sequence
 - Pat. Appln. SEQ ID NO 2461
 - Ceres seq_id 1503512
 - Location of start within SEQ ID NO 2459: at 39 nt.
- (C) Nomination and Annotation of Domains within Predicted Polypeptide(s)
 - (D) Related Amino Acid Sequences
 - Alignment No. 15115
 - gi No. 4091080
 - % Identity 70.7
 - Alignment Length 59
 - Location of Alignment in SEQ ID NO 2461: from 1 to 45

- (A) Polynucleotide Sequence
 - Pat. Appln. SEQ ID NO 2462
 - Ceres seq_id 1503522
 - (B) Polypeptide Sequence
 - Pat. Appln. SEQ ID NO 2463
 - Ceres seq_id 1503523
 - Location of start within SEQ ID NO 2462: at 87 nt.

- - (D) Related Amino Acid Sequences
 - Alignment No. 15116
 - gi No. 1173045
 - % Identity 87
 - Alignment Length 23
 - Location of Alignment in SEQ ID NO 2463: from 1 to 23
 - Alignment No. 15117
 - gi No. 1346945
 - % Identity 78.3
 - Alignment Length 23
 - Location of Alignment in SEQ ID NO 2463: from 1 to 23
 - Alignment No. 15118
 - gi No. 2281793
 - % Identity 70.6
 - Alignment Length 17
 - Location of Alignment in SEQ ID NO 2463: from 12 to 28
 - Alignment No. 15119
 - gi No. 2565332
 - % Identity 73.1
 - Alignment Length 26
 - Location of Alignment in SEQ ID NO 2463: from 3 to 28
 - Alignment No. 15120
 - gi No. 2996185
 - % Identity 91.3
 - Alignment Length 23
 - Location of Alignment in SEQ ID NO 2463: from 1 to 23
 - Alignment No. 15121
 - gi No. 3098458
 - % Identity 75
 - Alignment Length 28
 - Location of Alignment in SEQ ID NO 2463: from 1 to 28
 - Alignment No. 15122
 - gi No. 3845189
 - % Identity 73.9
 - Alignment Length 23
 - Location of Alignment in SEQ ID NO 2463: from 1 to 23
 - Alignment No. 15123
 - gi No. 400996
 - % Identity 91.3
 - Alignment Length 23
 - Location of Alignment in SEQ ID NO 2463: from 1 to 23
 - Alignment No. 15124
 - gi No. 4090257
 - % Identity 100
 - Alignment Length 23
 - Location of Alignment in SEQ ID NO 2463: from 1 to 23
 - Alignment No. 15125
 - gi No. 4455775
 - % Identity 71.4

- Alignment Length 28
- Location of Alignment in SEQ ID NO 2463: from 1 to 28
- Alignment No. 15126
- gi No. 4506643
- % Identity 91.3
- Alignment Length 23
- Location of Alignment in SEQ ID NO 2463: from 1 to 23
- Alignment No. 15127
- gi No. 4741896
- % Identity 100
- Alignment Length 23
- Location of Alignment in SEQ ID NO 2463: from 1 to 23
- Alignment No. 15128
- gi No. 5007072
- % Identity 100
- Alignment Length 15
- Location of Alignment in SEQ ID NO 2463: from 9 to 23
- (B) Polypeptide Sequence
 - Pat. Appln. SEQ ID NO 2464
 - Ceres seq id 1503524
 - Location of start within SEQ ID NO 2462: at 127 nt.
- (C) Nomination and Annotation of Domains within Predicted Polypeptide(s) $% \left(\frac{1}{2}\right) =\frac{1}{2}\left(\frac{1}{2}\right) +\frac{1}{2}\left(\frac{1}{2}\right) +\frac{$
 - (D) Related Amino Acid Sequences
 - (B) Polypeptide Sequence
 - Pat. Appln. SEQ ID NO 2465
 - Ceres seq id 1503525
 - Location of start within SEQ ID NO 2462: at 139 nt.
- (C) Nomination and Annotation of Domains within Predicted Polypeptide(s)
 - (D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 314734 (A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 2466
- Ceres seq_id 1503526
- (B) Polypeptide Sequence
 - Pat. Appln. SEQ ID NO 2467
 - Ceres seq_id 1503527
 - Location of start within SEQ ID NO 2466: at 1 nt.
- (C) Nomination and Annotation of Domains within Predicted Polypeptide(s) $\label{eq:continuous} % \begin{array}{c} \text{Polyperiod} \\ \text{Pol$
 - (D) Related Amino Acid Sequences
 - (B) Polypeptide Sequence
 - Pat. Appln. SEQ ID NO 2468
 - Ceres seq_id 1503528
 - Location of start within SEQ ID NO 2466: at 162 nt.
- (C) Nomination and Annotation of Domains within Predicted Polypeptide(s) $% \left(\frac{1}{2}\right) =\frac{1}{2}\left(\frac{1}{2}\right) +\frac{1}{2}\left(\frac{1}{2}\right) +\frac{$
 - Alignment No. 15129
 - Ribosomal protein L13

- Location within SEQ ID NO 2468: from 29 to 85 aa.
- (D) Related Amino Acid Sequences
- (B) Polypeptide Sequence
 - Pat. Appln. SEQ ID NO 2469
 - Ceres seq id 1503529
 - Location of start within SEQ ID NO 2466: at 352 nt.
- - (D) Related Amino Acid Sequences

- (A) Polynucleotide Sequence
 - Pat. Appln. SEQ ID NO 2470
 - Ceres seq id 1503550
 - (B) Polypeptide Sequence
 - Pat. Appln. SEQ ID NO 2471
 - Ceres seq_id 1503551
 - Location of start within SEQ ID NO 2470: at 1 nt.
- (C) Nomination and Annotation of Domains within Predicted Polypeptide(s) $\label{eq:condition} % \begin{array}{c} \text{Polyperiod} \\ \text{Poly$
 - (D) Related Amino Acid Sequences
 - Alignment No. 15130
 - gi No. 3935157
 - % Identity 71.5
 - Alignment Length 123
 - Location of Alignment in SEQ ID NO 2471: from 28 to 150
 - (B) Polypeptide Sequence
 - Pat. Appln. SEQ ID NO 2472
 - Ceres seq id 1503552
 - Location of start within SEQ ID NO 2470: at 42 nt.
- - (D) Related Amino Acid Sequences
 - (B) Polypeptide Sequence
 - Pat. Appln. SEQ ID NO 2473
 - Ceres seq_id 1503553
 - Location of start within SEQ ID NO 2470: at 73 nt.
- (C) Nomination and Annotation of Domains within Predicted Polypeptide(s) $% \left(\frac{1}{2}\right) =\frac{1}{2}\left(\frac{1}{2}\right) +\frac{1}{2}\left(\frac{1}{2}\right) +\frac{$
 - (D) Related Amino Acid Sequences
 - Alignment No. 15131
 - gi No. 3935157
 - % Identity 71.5
 - Alignment Length 123
 - Location of Alignment in SEQ ID NO 2473: from 4 to 126

- (A) Polynucleotide Sequence
 - Pat. Appln. SEQ ID NO 2474
 - Ceres seq_id 1503554
 - (B) Polypeptide Sequence
 - Pat. Appln. SEQ ID NO 2475
 - Ceres seq id 1503555

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- Location of start within SEQ ID NO 2474: at 3 nt.
- (C) Nomination and Annotation of Domains within Predicted Polypeptide(s) $% \left(\frac{1}{2}\right) =\frac{1}{2}\left(\frac{1}{2}\right) +\frac{1}{2}\left(\frac{1}{2}\right) +\frac{$
 - Alignment No. 15132
 - 7 transmembrane receptor (rhodopsin family)
 - Location within SEQ ID NO 2475: from 2 to 94 aa.
 - Alignment No. 15133
 - 7 transmembrane receptor (rhodopsin family)
 - Location within SEQ ID NO 2475: from 9 to 133 aa.
 - Alignment No. 15134
 - 7 transmembrane receptor (rhodopsin family)
 - Location within SEQ ID NO 2475: from 11 to 138 aa.
 - Alignment No. 15135
 - Assemblin (Peptidase family S21)
 - Location within SEQ ID NO 2475: from 3 to 114 aa.
 - Alignment No. 15136
 - Assemblin (Peptidase family S21)
 - Location within SEQ ID NO 2475: from 4 to 138 aa.
 - (D) Related Amino Acid Sequences
 - Alignment No. 15137
 - gi No. 2281102
 - % Identity 72.7
 - Alignment Length 11
 - Location of Alignment in SEQ ID NO 2475: from 128 to 138
 - (B) Polypeptide Sequence
 - Pat. Appln. SEQ ID NO 2476
 - Ceres seq id 1503556
 - Location of start within SEQ ID NO 2474: at 60 nt.
- - Alignment No. 15138
 - 7 transmembrane receptor (rhodopsin family)
 - Location within SEQ ID NO 2476: from 1 to 75 aa.
 - Alignment No. 15139
 - 7 transmembrane receptor (rhodopsin family)
 - Location within SEQ ID NO 2476: from 1 to 114 aa.
 - Alignment No. 15140
 - 7 transmembrane receptor (rhodopsin family)
 - Location within SEQ ID NO 2476: from 1 to 119 aa.
 - Alignment No. 15141
 - Assemblin (Peptidase family S21)
 - Location within SEQ ID NO 2476: from 1 to 95 aa.
 - Alignment No. 15142
 - Assemblin (Peptidase family S21)
 - Location within SEQ ID NO 2476: from 1 to 119 aa.
 - (D) Related Amino Acid Sequences
 - Alignment No. 15143
 - gi No. 2281102

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- % Identity 72.7
- Alignment Length 11
- Location of Alignment in SEQ ID NO 2476: from 109 to 119
- (B) Polypeptide Sequence
 - Pat. Appln. SEQ ID NO 2477
 - Ceres seq id 1503557
 - Location of start within SEQ ID NO 2474: at 118 nt.
- (C) Nomination and Annotation of Domains within Predicted Polypeptide(s)
 - (D) Related Amino Acid Sequences
 - Alignment No. 15144
 - gi No. 109944
 - % Identity 71.4
 - Alignment Length 14
 - Location of Alignment in SEQ ID NO 2477: from 74 to 87
 - Alignment No. 15145

 - gi No. 1350911
 % Identity 71.4
 - Alignment Length 14
 - Location of Alignment in SEQ ID NO 2477: from 74 to 87
 - Alignment No. 15146
 - gi No. 1350912
 - % Identity 71.4
 - Alignment Length 14
 - Location of Alignment in SEQ ID NO 2477: from 74 to 87
 - Alignment No. 15147
 - gi No. 200880
 - % Identity 71.4
 - Alignment Length 14
 - Location of Alignment in SEQ ID NO 2477: from 74 to 87
 - Alignment No. 15148
 - gi No. 2564955
 - % Identity 72.7
 - Alignment Length 11
 - Location of Alignment in SEQ ID NO 2477: from 76 to 86
 - Alignment No. 15149
 - qi No. 337720
 - % Identity 71.4
 - Alignment Length 14
 - Location of Alignment in SEQ ID NO 2477: from 74 to 87
 - Alignment No. 15150
 - qi No. 483195
 - % Identity 71.4
 - Alignment Length 14
 - Location of Alignment in SEQ ID NO 2477: from 74 to 87
 - Alignment No. 15151
 - gi No. 542994
 - % Identity 71.4
 - Alignment Length 14
 - Location of Alignment in SEQ ID NO 2477: from 74 to 87

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- (A) Polynucleotide Sequence
 - Pat. Appln. SEQ ID NO 2478
 - Ceres seq_id 1503569
 - (B) Polypeptide Sequence
 - Pat. Appln. SEQ ID NO 2479
 - Ceres seq_id 1503570
 - Location of start within SEQ ID NO 2478: at 1 nt.
- (C) Nomination and Annotation of Domains within Predicted Polypeptide(s)
 - (D) Related Amino Acid Sequences
 - Alignment No. 15152
 - gi No. 4455361
 - % Identity 72.2
 - Alignment Length 54
 - Location of Alignment in SEQ ID NO 2479: from 34 to 87
 - (B) Polypeptide Sequence
 - Pat. Appln. SEQ ID NO 2480
 - Ceres seq id 1503571
 - Location of start within SEQ ID NO 2478: at 100 nt.
- - (D) Related Amino Acid Sequences
 - Alignment No. 15153
 - gi No. 4455361
 - % Identity 72.2
 - Alignment Length 54
 - Location of Alignment in SEQ ID NO 2480: from 1 to 54
 - (B) Polypeptide Sequence
 - Pat. Appln. SEQ ID NO 2481
 - Ceres seq_id 1503572
 - Location of start within SEQ ID NO 2478: at 142 nt.
- - (D) Related Amino Acid Sequences
 - Alignment No. 15154
 - gi No. 4455361
 - % Identity 72.2
 - Alignment Length 54
 - Location of Alignment in SEQ ID NO 2481: from 1 to 40

- (A) Polynucleotide Sequence
- Pat. Appln. SEQ ID NO 2482
 - Ceres seq_id 1503585
 - (B) Polypeptide Sequence
 - Pat. Appln. SEQ ID NO 2483
 - Ceres seq_id 1503586
 - Location of start within SEQ ID NO 2482: at 87 nt.
- (C) Nomination and Annotation of Domains within Predicted Polypeptide(s)
 - Alignment No. 15155
 - WD domain, G-beta repeat
 - Location within SEQ ID NO 2483: from 20 to 58 aa.
 - (D) Related Amino Acid Sequences

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- Alignment No. 15156
- gi No. 1143814
- % Identity 74.8
- Alignment Length 111
- Location of Alignment in SEQ ID NO 2483: from 1 to 108
- Alignment No. 15157
- gi No. 1346106
- % Identity 74.8
- Alignment Length 112
- Location of Alignment in SEQ ID NO 2483: from 1 to 108
- Alignment No. 15158
- gi No. 1346107
- % Identity 99.1
- Alignment Length 111
- Location of Alignment in SEQ ID NO 2483: from 1 to 108
- Alignment No. 15159
- gi No. 2935698
- % Identity 91.1
- Alignment Length 112
- Location of Alignment in SEQ ID NO 2483: from 1 to 108
- Alignment No. 15160
- gi No. 3023832
- % Identity 73.9
- Alignment Length 111
- Location of Alignment in SEQ ID NO 2483: from 1 to 108
- Alignment No. 15161
- gi No. 3023839
- % Identity 74.8
- Alignment Length 111
- Location of Alignment in SEQ ID NO 2483: from 1 to 108
- Alignment No. 15162
- gi No. 3023841
- % Identity 73
- Alignment Length 111
- Location of Alignment in SEQ ID NO 2483: from 1 to 108
- Alignment No. 15163
- gi No. 3023842
- % Identity 75.7
- Alignment Length 111
- Location of Alignment in SEQ ID NO 2483: from 1 to 108
- Alignment No. 15164
- gi No. 3023843
- % Identity 92.8
- Alignment Length 111
- Location of Alignment in SEQ ID NO 2483: from 1 to 108
- Alignment No. 15165
- gi No. 3023859
- % Identity 74.8
- Alignment Length 111
- Location of Alignment in SEQ ID NO 2483: from 1 to 108
- Alignment No. 15166

- gi No. 4929352
- % Identity 76.6
- Alignment Length 111
- Location of Alignment in SEQ ID NO 2483: from 1 to 108
- (B) Polypeptide Sequence
 - Pat. Appln. SEQ ID NO 2484
 - Ceres seg id 1503587
 - Location of start within SEQ ID NO 2482: at 261 nt.
- - (D) Related Amino Acid Sequences
 - Alignment No. 15167
 - gi No. 1143814
 - % Identity 74.8
 - Alignment Length 111
 - Location of Alignment in SEQ ID NO 2484: from 1 to 50
 - Alignment No. 15168
 - gi No. 1346106
 - % Identity 74.8
 - Alignment Length 112
 - Location of Alignment in SEQ ID NO 2484: from 1 to 50
 - Alignment No. 15169
 - gi No. 1346107
 - % Identity 99.1
 - Alignment Length 111
 - Location of Alignment in SEQ ID NO 2484: from 1 to 50
 - Alignment No. 15170
 - gi No. 2935698
 - % Identity 91.1
 - Alignment Length 112
 - Location of Alignment in SEQ ID NO 2484: from 1 to 50
 - Alignment No. 15171
 - gi No. 3023832
 - % Identity 73.9
 - Alignment Length 111
 - Location of Alignment in SEQ ID NO 2484: from 1 to 50
 - Alignment No. 15172
 - gi No. 3023839
 - % Identity 74.8
 - Alignment Length 111
 - Location of Alignment in SEQ ID NO 2484: from 1 to 50
 - Alignment No. 15173
 - gi No. 3023841
 - % Identity 73
 - Alignment Length 111
 - Location of Alignment in SEQ ID NO 2484: from 1 to 50
 - Alignment No. 15174
 - gi No. 3023842
 - % Identity 75.7
 - Alignment Length 111
 - Location of Alignment in SEQ ID NO 2484: from 1 to 50

- Alignment No. 15175

- gi No. 3023843
- % Identity 92.8
- Alignment Length 111
- Location of Alignment in SEQ ID NO 2484: from 1 to 50
- Alignment No. 15176
- gi No. 3023859
- % Identity 74.8
- Alignment Length 111
- Location of Alignment in SEQ ID NO 2484: from 1 to 50
- Alignment No. 15177
- gi No. 4929352
- % Identity 76.6
- Alignment Length 111
- Location of Alignment in SEQ ID NO 2484: from 1 to 50

- (A) Polynucleotide Sequence
 - Pat. Appln. SEQ ID NO 2485
 - Ceres seq_id 1503588
 - (B) Polypeptide Sequence
 - Pat. Appln. SEQ ID NO 2486
 - Ceres seq_id 1503589
 - Location of start within SEQ ID NO 2485: at 184 nt.
- (C) Nomination and Annotation of Domains within Predicted Polypeptide(s) $\label{eq:continuous}$
 - Alignment No. 15178
 - Ubiquitin-conjugating enzyme
 - Location within SEQ ID NO 2486: from 1 to 100 aa.
 - (D) Related Amino Acid Sequences
 - Alignment No. 15179
 - gi No. 1142614
 - % Identity 85.2
 - Alignment Length 108
 - Location of Alignment in SEQ ID NO 2486: from 1 to 100
 - Alignment No. 15180
 - gi No. 1174848
 - % Identity 76.1
 - Alignment Length 113
 - Location of Alignment in SEQ ID NO 2486: from 1 to 98
 - Alignment No. 15181
 - gi No. 1174849
 - % Identity 79.6
 - Alignment Length 113
 - Location of Alignment in SEQ ID NO 2486: from 1 to 100
 - Alignment No. 15182
 - qi No. 136643
 - % Identity 77.4
 - Alignment Length 115
 - Location of Alignment in SEQ ID NO 2486: from 1 to 100
 - Alignment No. 15183
 - gi No. 136645
 - % Identity 75.7

- Alignment Length 115
- Location of Alignment in SEQ ID NO 2486: from 1 to 100
- Alignment No. 15184
- gi No. 136646
- % Identity 76.5
- Alignment Length 115
- Location of Alignment in SEQ ID NO 2486: from 1 to 100
- Alignment No. 15185
- gi No. 2130087
- % Identity 81.4
- Alignment Length 118
- Location of Alignment in SEQ ID NO 2486: from 1 to 100
- Alignment No. 15186
- gi No. 2130088
- % Identity 80.5
- Alignment Length 118
- Location of Alignment in SEQ ID NO 2486: from 1 to 100
- Alignment No. 15187
- gi No. 2136339
- % Identity 78.3
- Alignment Length 115
- Location of Alignment in SEQ ID NO 2486: from 1 to 100
- Alignment No. 15188
- gi No. 2501431
- % Identity 75.2
- Alignment Length 113
- Location of Alignment in SEQ ID NO 2486: from 1 to 100
- Alignment No. 15189
- gi No. 2612962
- % Identity 75.3
- Alignment Length 89
- Location of Alignment in SEQ ID NO 2486: from 1 to 74
- Alignment No. 15190
- gi No. 2668744
- % Identity 90.3
- Alignment Length 113
- Location of Alignment in SEQ ID NO 2486: from 1 to 100
- Alignment No. 15191
- gi No. 3043432
- % Identity 95.2
- Alignment Length 42
- Location of Alignment in SEQ ID NO 2486: from 59 to 100
- Alignment No. 15192
- gi No. 3323498
- % Identity 77.4
- Alignment Length 115
- Location of Alignment in SEQ ID NO 2486: from 1 to 100
- Alignment No. 15193
- gi No. 3915190
- % Identity 93.3
- Alignment Length 105

- Location of Alignment in SEQ ID NO 2486: from 1 to 100
- Alignment No. 15194
- gi No. 4097684
- % Identity 82
- Alignment Length 89
- Location of Alignment in SEQ ID NO 2486: from 12 to 100
- Alignment No. 15195
- gi No. 4100646
- % Identity 81.7
- Alignment Length 115
- Location of Alignment in SEQ ID NO 2486: from 1 to 100
- Alignment No. 15196
- gi No. 441457
- % Identity 88.5
- Alignment Length 113
- Location of Alignment in SEQ ID NO 2486: from 1 to 100
- Alignment No. 15197
- gi No. 4433363
- % Identity 94.2
- Alignment Length 69
- Location of Alignment in SEQ ID NO 2486: from 32 to 100
- Alignment No. 15198
- gi No. 4507773
- % Identity 74.8
- Alignment Length 115
- Location of Alignment in SEQ ID NO 2486: from 1 to 100 $\,$
- Alignment No. 15199
- gi No. 4507775
- % Identity 78.3
- Alignment Length 115
- Location of Alignment in SEQ ID NO 2486: from 1 to 100 $\,$
- Alignment No. 15200
- gi No. 4507777
- % Identity 78.3
- Alignment Length 115
- Location of Alignment in SEQ ID NO 2486: from 1 to 100
- Alignment No. 15201
- gi No. 456568
- % Identity 88.5
- Alignment Length 113
- Location of Alignment in SEQ ID NO 2486: from 1 to 100
- Alignment No. 15202
- gi No. 4581117
- % Identity 85.2
- Alignment Length 115
- Location of Alignment in SEQ ID NO 2486: from 1 to 100
- Alignment No. 15203
- gi No. 4583656
- % Identity 73.9
- Alignment Length 111
- Location of Alignment in SEQ ID NO 2486: from 1 to 98

- Alignment No. 15204 - gi No. 464979 - % Identity 76.5 - Alignment Length 115 - Location of Alignment in SEQ ID NO 2486: from 1 to 100 - Alignment No. 15205 - gi No. 464981 - % Identity 89.4 - Alignment Length 113 - Location of Alignment in SEQ ID NO 2486: from 1 to 100 - Alignment No. 15206 - qi No. 464985 - % Identity 87.6 - Alignment Length 113 - Location of Alignment in SEQ ID NO 2486: from 1 to 100 - Alignment No. 15207 - gi No. 464986 - % Identity 89.4 - Alignment Length 113 - Location of Alignment in SEQ ID NO 2486: from 1 to 100 - Alignment No. 15208 - gi No. 464987 - % Identity 89.4 - Alignment Length 113 - Location of Alignment in SEQ ID NO 2486: from 1 to 100 - Alignment No. 15209 - gi No. 464988 - % Identity 91.9 - Alignment Length 99 - Location of Alignment in SEQ ID NO 2486: from 2 to 100 - Alignment No. 15210 - gi No. 477134 - % Identity 76.5 - Alignment Length 115 - Location of Alignment in SEQ ID NO 2486: from 1 to 100 - Alignment No. 15211 - gi No. 4868140 - % Identity 78.3 - Alignment Length 115

- Location of Alignment in SEQ ID NO 2486: from 1 to 100

- Location of Alignment in SEQ ID NO 2486: from 12 to 100

- (B) Polypeptide Sequence
 - Pat. Appln. SEQ ID NO 2487

- Alignment No. 15212 - gi No. 4868141 - % Identity 79.8 - Alignment Length 89

- Ceres seq_id 1503590
- Location of start within SEQ ID NO 2485: at 208 nt.

- - Alignment No. 15213
 - Ubiquitin-conjugating enzyme
 - Location within SEQ ID NO 2487: from 1 to 92 aa.
 - (D) Related Amino Acid Sequences
 - Alignment No. 15214
 - gi No. 1142614
 - % Identity 85.2
 - Alignment Length 108
 - Location of Alignment in SEQ ID NO 2487: from 1 to 92
 - Alignment No. 15215
 - gi No. 1174848
 - % Identity 76.1
 - Alignment Length 113
 - Location of Alignment in SEQ ID NO 2487: from 1 to 90
 - Alignment No. 15216
 - qi No. 1174849
 - % Identity 79.6
 - Alignment Length 113
 - Location of Alignment in SEQ ID NO 2487: from 1 to 92
 - Alignment No. 15217
 - gi No. 136643
 - % Identity 77.4
 - Alignment Length 115
 - Location of Alignment in SEQ ID NO 2487: from 1 to 92
 - Alignment No. 15218
 - gi No. 136645
 - % Identity 75.7
 - Alignment Length 115
 - Location of Alignment in SEQ ID NO 2487: from 1 to 92
 - Alignment No. 15219
 - gi No. 136646
 - % Identity 76.5
 - Alignment Length 115
 - Location of Alignment in SEQ ID NO 2487: from 1 to 92
 - Alignment No. 15220
 - gi No. 2130087
 - % Identity 81.4
 - Alignment Length 118
 - Location of Alignment in SEQ ID NO 2487: from 1 to 92
 - Alignment No. 15221
 - gi No. 2130088
 - % Identity 80.5
 - Alignment Length 118
 - Location of Alignment in SEQ ID NO 2487: from 1 to 92
 - Alignment No. 15222
 - gi No. 2136339
 - % Identity 78.3
 - Alignment Length 115
 - Location of Alignment in SEQ ID NO 2487: from 1 to 92

- Alignment No. 15223
- gi No. 2501431
- % Identity 75.2
- Alignment Length 113
- Location of Alignment in SEQ ID NO 2487: from 1 to 92
- Alignment No. 15224
- gi No. 2612962
- % Identity 75.3
- Alignment Length 89
- Location of Alignment in SEQ ID NO 2487: from 1 to 66
- Alignment No. 15225
- gi No. 2668744
- % Identity 90.3
- Alignment Length 113
- Location of Alignment in SEQ ID NO 2487: from 1 to 92
- Alignment No. 15226
- gi No. 3043432
- % Identity 95.2
- Alignment Length 42
- Location of Alignment in SEQ ID NO 2487: from 51 to 92
- Alignment No. 15227
- gi No. 3323498
- % Identity 77.4
- Alignment Length 115
- Location of Alignment in SEQ ID NO 2487: from 1 to 92
- Alignment No. 15228
- gi No. 3915190
- % Identity 93.3
- Alignment Length 105
- Location of Alignment in SEQ ID NO 2487: from 1 to 92
- Alignment No. 15229
- gi No. 4097684
- % Identity 82
- Alignment Length 89
- Location of Alignment in SEQ ID NO 2487: from 4 to 92
- Alignment No. 15230
- gi No. 4100646
- % Identity 81.7
- Alignment Length 115
- Location of Alignment in SEQ ID NO 2487: from 1 to 92
- Alignment No. 15231
- gi No. 441457
- % Identity 88.5
- Alignment Length 113
- Location of Alignment in SEQ ID NO 2487: from 1 to 92
- Alignment No. 15232
- gi No. 4433363
- % Identity 94.2
- Alignment Length 69
- Location of Alignment in SEQ ID NO 2487: from 24 to 92
- Alignment No. 15233

- gi No. 4507773
- % Identity 74.8
- Alignment Length 115
- Location of Alignment in SEQ ID NO 2487: from 1 to 92
- Alignment No. 15234
- gi No. 4507775
- % Identity 78.3
- Alignment Length 115
- Location of Alignment in SEQ ID NO 2487: from 1 to 92
- Alignment No. 15235
- gi No. 4507777
- % Identity 78.3
- Alignment Length 115
- Location of Alignment in SEQ ID NO 2487: from 1 to 92
- Alignment No. 15236
- gi No. 456568
- % Identity 88.5
- Alignment Length 113
- Location of Alignment in SEQ ID NO 2487: from 1 to 92
- Alignment No. 15237
- gi No. 4581117
- % Identity 85.2
- Alignment Length 115
- Location of Alignment in SEQ ID NO 2487: from 1 to 92
- Alignment No. 15238
- gi No. 4583656
- % Identity 73.9
- Alignment Length 111
- Location of Alignment in SEQ ID NO 2487: from 1 to 90 $\,$
- Alignment No. 15239
- gi No. 464979
- % Identity 76.5
- Alignment Length 115
- Location of Alignment in SEQ ID NO 2487: from 1 to 92
- Alignment No. 15240
- gi No. 464981
- % Identity 89.4
- Alignment Length 113
- Location of Alignment in SEQ ID NO 2487: from 1 to 92
- Alignment No. 15241
- gi No. 464985
- % Identity 87.6
- Alignment Length 113
- Location of Alignment in SEQ ID NO 2487: from 1 to 92
- Alignment No. 15242
- gi No. 464986
- % Identity 89.4
- Alignment Length 113
- Location of Alignment in SEQ ID NO 2487: from 1 to 92
- Alignment No. 15243
- gi No. 464987

- % Identity 89.4
- Alignment Length 113
- Location of Alignment in SEQ ID NO 2487: from 1 to 92
- Alignment No. 15244
- gi No. 464988
- % Identity 91.9
- Alignment Length 99
- Location of Alignment in SEQ ID NO 2487: from 1 to 92
- Alignment No. 15245
- gi No. 477134
- % Identity 76.5
- Alignment Length 115
- Location of Alignment in SEQ ID NO 2487: from 1 to 92
- Alignment No. 15246
- gi No. 4868140
- % Identity 78.3
- Alignment Length 115
- Location of Alignment in SEQ ID NO 2487: from 1 to 92
- Alignment No. 15247
- gi No. 4868141
- % Identity 79.8
- Alignment Length 89
- Location of Alignment in SEQ ID NO 2487: from 4 to 92

- (A) Polynucleotide Sequence
 - Pat. Appln. SEQ ID NO 2488
 - Ceres seq_id 1503591
 - (B) Polypeptide Sequence
 - Pat. Appln. SEQ ID NO 2489
 - Ceres seq id 1503592
 - Location of start within SEQ ID NO 2488: at 2 nt.
- (C) Nomination and Annotation of Domains within Predicted Polypeptide(s) $% \left(\frac{1}{2}\right) =\frac{1}{2}\left(\frac{1}{2}\right) +\frac{1}{2}\left(\frac{1}{2}\right) +\frac{$
 - Alignment No. 15248
 - Glycosyl hydrolases family 16
 - Location within SEQ ID NO 2489: from 1 to 115 aa.
 - (D) Related Amino Acid Sequences
 - Alignment No. 15249
 - gi No. 2129770
 - % Identity 70.9
 - Alignment Length 127
 - Location of Alignment in SEQ ID NO 2489: from 1 to 126
 - Alignment No. 15250
 - gi No. 2154609
 - % Identity 70.9
 - Alignment Length 127
 - Location of Alignment in SEQ ID NO 2489: from 1 to 126
 - Alignment No. 15251
 - gi No. 5533313
 - % Identity 70.9
 - Alignment Length 127
 - Location of Alignment in SEQ ID NO 2489: from 1 to 126

- (B) Polypeptide Sequence
 - Pat. Appln. SEQ ID NO 2490
 - Ceres seq id 1503593
 - Location of start within SEQ ID NO 2488: at 3 nt.
- - Alignment No. 15252
 - Mucin-like glycoprotein
 - Location within SEQ ID NO 2490: from 1 to 126 aa.
 - (D) Related Amino Acid Sequences

- (A) Polynucleotide Sequence
 - Pat. Appln. SEQ ID NO 2491
 - Ceres seq_id 1503594
 - (B) Polypeptide Sequence
 - Pat. Appln. SEQ ID NO 2492
 - Ceres seq_id 1503595
 - Location of start within SEQ ID NO 2491: at 2 nt.
- (C) Nomination and Annotation of Domains within Predicted Polypeptide(s)
 - Alignment No. 15253
 - Ubiquitin-conjugating enzyme
 - Location within SEQ ID NO 2492: from 1 to 59 aa.
 - (D) Related Amino Acid Sequences
 - Alignment No. 15254
 - gi No. 4006890
 - % Identity 84.7
 - Alignment Length 59
 - Location of Alignment in SEQ ID NO 2492: from 1 to 59
 - Alignment No. 15255
 - gi No. 4217999
 - % Identity 84.7
 - Alignment Length 59
 - Location of Alignment in SEQ ID NO 2492: from 1 to 59
 - (B) Polypeptide Sequence
 - Pat. Appln. SEQ ID NO 2493
 - Ceres seq_id 1503596
 - Location of start within SEQ ID NO 2491: at 224 nt.
- (C) Nomination and Annotation of Domains within Predicted Polypeptide(s) $% \left(\frac{1}{2}\right) =\frac{1}{2}\left(\frac{1}{2}\right) +\frac{1}{2}\left(\frac{1}{2}\right) +\frac{$
 - (D) Related Amino Acid Sequences
 - (B) Polypeptide Sequence
 - Pat. Appln. SEQ ID NO 2494
 - Ceres seq_id 1503597
 - Location of start within SEQ ID NO 2491: at 246 nt.
- - (D) Related Amino Acid Sequences

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- (A) Polynucleotide Sequence
 - Pat. Appln. SEQ ID NO 2495
 - Ceres seq_id 1503600
 - (B) Polypeptide Sequence
 - Pat. Appln. SEQ ID NO 2496
 - Ceres seq id 1503601
 - Location of start within SEQ ID NO 2495: at 3 nt.
- - (D) Related Amino Acid Sequences
 - Alignment No. 15256
 - gi No. 1173018
 - % Identity 100
 - Alignment Length 15
 - Location of Alignment in SEQ ID NO 2496: from 35 to 49
 - Alignment No. 15257
 - gi No. 132849
 - % Identity 100
 - Alignment Length 15
 - Location of Alignment in SEQ ID NO 2496: from 35 to 49
 - Alignment No. 15258
 - gi No. 266944
 - % Identity 100
 - Alignment Length 15
 - Location of Alignment in SEQ ID NO 2496: from 35 to 49
 - Alignment No. 15259
 - qi No. 2961372
 - % Identity 100
 - Alignment Length 15
 - Location of Alignment in SEQ ID NO 2496: from 35 to 49
 - Alignment No. 15260
 - gi No. 3088346
 - % Identity 73.3
 - Alignment Length 15
 - Location of Alignment in SEQ ID NO 2496: from 35 to 49
 - Alignment No. 15261
 - gi No. 4406816
 - % Identity 100
 - Alignment Length 15
 - Location of Alignment in SEQ ID NO 2496: from 35 to 49
 - (B) Polypeptide Sequence
 - Pat. Appln. SEQ ID NO 2497
 - Ceres seq_id 1503602
 - Location of start within SEQ ID NO 2495: at 79 nt.
- (C) Nomination and Annotation of Domains within Predicted Polypeptide(s) $\label{eq:polypeptide}$
 - Alignment No. 15262
 - Ribosomal Proteins L2
 - Location within SEQ ID NO 2497: from 25 to 110 aa.
 - (D) Related Amino Acid Sequences
 - Alignment No. 15263
 - gi No. 132849

- % Identity 75.9
- Alignment Length 112
- Location of Alignment in SEQ ID NO 2497: from 1 to 110
- Alignment No. 15264
- gi No. 266944
- % Identity 77.7
- Alignment Length 112
- Location of Alignment in SEQ ID NO 2497: from 1 to 110
- Alignment No. 15265
- gi No. 2961372
- % Identity 74.1
- Alignment Length 112
- Location of Alignment in SEQ ID NO 2497: from 1 to 110
- Alignment No. 15266
- gi No. 4406816
- % Identity 75
- Alignment Length 112
- Location of Alignment in SEQ ID NO 2497: from 1 to 110

- (A) Polynucleotide Sequence
 - Pat. Appln. SEQ ID NO 2498
 - Ceres seq_id 1503615
 - (B) Polypeptide Sequence
 - Pat. Appln. SEQ ID NO 2499
 - Ceres seq_id 1503616
 - Location of start within SEQ ID NO 2498: at 1 nt.
- - (D) Related Amino Acid Sequences
 - Alignment No. 15267
 - gi No. 481728
 - % Identity 81.8
 - Alignment Length 11
 - Location of Alignment in SEQ ID NO 2499: from 76 to 86
 - Alignment No. 15268
 - gi No. 481728
 - % Identity 75
 - Alignment Length 12
 - Location of Alignment in SEQ ID NO 2499: from 76 to 86
 - (B) Polypeptide Sequence
 - Pat. Appln. SEQ ID NO 2500
 - Ceres seq_id 1503617
 - Location of start within SEQ ID NO 2498: at 2 nt.
- (C) Nomination and Annotation of Domains within Predicted Polypeptide(s) $\label{eq:condition} % \begin{array}{c} \text{Polyperiod} \\ \text{Poly$
 - (D) Related Amino Acid Sequences
 - Alignment No. 15269
 - gi No. 3941736
 - % Identity 75
 - Alignment Length 12
 - Location of Alignment in SEQ ID NO 2500: from 93 to 104
 - Alignment No. 15270

- gi No. 4337109
- % Identity 75
- Alignment Length 12
- Location of Alignment in SEQ ID NO 2500: from 93 to 104
- Alignment No. 15271
- gi No. 4758110
- % Identity 75
- Alignment Length 12
- Location of Alignment in SEQ ID NO 2500: from 93 to 104
- Alignment No. 15272
- gi No. 5668598
- % Identity 75
- Alignment Length 12
- Location of Alignment in SEQ ID NO 2500: from 93 to 104
- Alignment No. 15273
- gi No. 5668598
- % Identity 75
- Alignment Length 12
- Location of Alignment in SEQ ID NO 2500: from 95 to 106
- (B) Polypeptide Sequence
 - Pat. Appln. SEQ ID NO 2501
 - Ceres seq id 1503618
 - Location of start within SEQ ID NO 2498: at 3 nt.
- (C) Nomination and Annotation of Domains within Predicted Polypeptide(s)
 - (D) Related Amino Acid Sequences

- (A) Polynucleotide Sequence
 - Pat. Appln. SEQ ID NO 2502
 - Ceres seq_id 1503621
 - (B) Polypeptide Sequence
 - Pat. Appln. SEQ ID NO 2503
 - Ceres seq_id 1503622
 - Location of start within SEQ ID NO 2502: at 1 nt.
- (C) Nomination and Annotation of Domains within Predicted Polypeptide(s)
 - Alignment No. 15274
 - Putative GTP-ase activating protein for Arf
 - Location within SEQ ID NO 2503: from 74 to 132 aa.
 - (D) Related Amino Acid Sequences
 - Alignment No. 15275
 - gi No. 3236238
 - % Identity 83.1
 - Alignment Length 59
 - Location of Alignment in SEQ ID NO 2503: from 74 to 132
 - (B) Polypeptide Sequence
 - Pat. Appln. SEQ ID NO 2504
 - Ceres seq id 1503623
 - Location of start within SEQ ID NO 2502: at 3 nt.

- (D) Related Amino Acid Sequences
- (B) Polypeptide Sequence
 - Pat. Appln. SEQ ID NO 2505
 - Ceres seq_id 1503624
 - Location of start within SEQ ID NO 2502: at 140 nt.
- (C) Nomination and Annotation of Domains within Predicted Polypeptide(s)
 - (D) Related Amino Acid Sequences

- (A) Polynucleotide Sequence
 - Pat. Appln. SEQ ID NO 2506
 - Ceres seq_id 1503662
 - (B) Polypeptide Sequence
 - Pat. Appln. SEQ ID NO 2507
 - Ceres seq id 1503663
 - Location of start within SEQ ID NO 2506: at 2 nt.
- (C) Nomination and Annotation of Domains within Predicted Polypeptide(s)
 - (D) Related Amino Acid Sequences
 - Alignment No. 15276
 - gi No. 3123264
 - % Identity 75.5
 - Alignment Length 49
 - Location of Alignment in SEQ ID NO 2507: from 81 to 128
 - (B) Polypeptide Sequence
 - Pat. Appln. SEQ ID NO 2508
 - Ceres seq_id 1503664
 - Location of start within SEQ ID NO 2506: at 3 nt.
- - (D) Related Amino Acid Sequences
 - Alignment No. 15277
 - gi No. 3123264
 - % Identity 70.5
 - Alignment Length 61
 - Location of Alignment in SEQ ID NO 2508: from 26 to 86
 - Alignment No. 15278
 - gi No. 498906
 - % Identity 70.5
 - Alignment Length 61
 - Location of Alignment in SEQ ID NO 2508: from 26 to 86
 - Alignment No. 15279
 - gi No. 730547
 - % Identity 75.4
 - Alignment Length 61
 - Location of Alignment in SEQ ID NO 2508: from 26 to 86
 - (B) Polypeptide Sequence
 - Pat. Appln. SEQ ID NO 2509
 - Ceres seq_id 1503665
 - Location of start within SEQ ID NO 2506: at 78 nt.

- - (D) Related Amino Acid Sequences
 - Alignment No. 15280
 - gi No. 3123264
 - % Identity 70.5
 - Alignment Length 61
 - Location of Alignment in SEQ ID NO 2509: from 1 to 61
 - Alignment No. 15281
 - gi No. 498906
 - % Identity 70.5
 - Alignment Length 61
 - Location of Alignment in SEQ ID NO 2509: from 1 to 61
 - Alignment No. 15282
 - gi No. 730547
 - % Identity 75.4
 - Alignment Length 61
 - Location of Alignment in SEQ ID NO 2509: from 1 to 61

- (A) Polynucleotide Sequence
 - Pat. Appln. SEQ ID NO 2510
 - Ceres seq_id 1503670
 - (B) Polypeptide Sequence
 - Pat. Appln. SEQ ID NO 2511
 - Ceres seq_id 1503671
 - Location of start within SEQ ID NO 2510: at 104 nt.
- - (D) Related Amino Acid Sequences
 - Alignment No. 15283
 - gi No. 1170395
 - % Identity 73.3
 - Alignment Length 15
 - Location of Alignment in SEQ ID NO 2511: from 29 to 43
 - Alignment No. 15284
 - gi No. 1170396
 - % Identity 73.3
 - Alignment Length 15
 - Location of Alignment in SEQ ID NO 2511: from 29 to 43
 - Alignment No. 15285
 - gi No. 1170396
 - % Identity 70.6
 - Alignment Length 17
 - Location of Alignment in SEQ ID NO 2511: from 29 to 45
 - Alignment No. 15286
 - gi No. 1170397
 - % Identity 73.3
 - Alignment Length 15
 - Location of Alignment in SEQ ID NO 2511: from 29 to 43
 - Alignment No. 15287
 - gi No. 1170397
 - % Identity 70.6
 - Alignment Length 17

- Location of Alignment in SEQ ID NO 2511: from 29 to 45
- Alignment No. 15288
- gi No. 1170398
- % Identity 73.3
- Alignment Length 15
- Location of Alignment in SEQ ID NO 2511: from 29 to 43
- Alignment No. 15289
- gi No. 1170398
- % Identity 70.6
- Alignment Length 17
- Location of Alignment in SEQ ID NO 2511: from 29 to 45

- (A) Polynucleotide Sequence
 - Pat. Appln. SEQ ID NO 2512
 - Ceres seq_id 1503697
 - (B) Polypeptide Sequence
 - Pat. Appln. SEQ ID NO 2513
 - Ceres seq id 1503698
 - Location of start within SEQ ID NO 2512: at 73 nt.
- (C) Nomination and Annotation of Domains within Predicted Polypeptide(s) $% \left(\frac{1}{2}\right) =\frac{1}{2}\left(\frac{1}{2}\right) +\frac{1}{2}\left(\frac{1}{2}\right) +\frac{$
 - Alignment No. 15290
 - Copper amine oxidase
 - Location within SEQ ID NO 2513: from 1 to 123 aa.
 - (D) Related Amino Acid Sequences
 - Alignment No. 15291
 - gi No. 4559342
 - % Identity 93.1
 - Alignment Length 131
 - Location of Alignment in SEQ ID NO 2513: from 1 to 122
 - Alignment No. 15292
 - gi No. 4567319
 - % Identity 93.1
 - Alignment Length 131
 - Location of Alignment in SEQ ID NO 2513: from 1 to 122
 - Alignment No. 15293
 - gi No. 5230728
 - % Identity 90.8
 - Alignment Length 131
 - Location of Alignment in SEQ ID NO 2513: from 1 to 122

- (A) Polynucleotide Sequence
 - Pat. Appln. SEQ ID NO 2514
 - Ceres seq_id 1503703
 - (B) Polypeptide Sequence
 - Pat. Appln. SEQ ID NO 2515
 - Ceres seq_id 1503704
 - Location of start within SEQ ID NO 2514: at 1 nt.
- (C) Nomination and Annotation of Domains within Predicted Polypeptide(s)
 - (D) Related Amino Acid Sequences

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- (B) Polypeptide Sequence
 - Pat. Appln. SEQ ID NO 2516
 - Ceres seq_id 1503705
 - Location of start within SEQ ID NO 2514: at 3 nt.
- - (D) Related Amino Acid Sequences
 - Alignment No. 15294
 - gi No. 4512664
 - % Identity 77.8
 - Alignment Length 45
 - Location of Alignment in SEQ ID NO 2516: from 35 to 79
 - Alignment No. 15295
 - gi No. 4874278
 - % Identity 74
 - Alignment Length 77
 - Location of Alignment in SEQ ID NO 2516: from 75 to 151
 - Alignment No. 15296
 - gi No. 4902470
 - % Identity 74
 - Alignment Length 77
 - Location of Alignment in SEQ ID NO 2516: from 75 to 151
 - Alignment No. 15297
 - gi No. 4902877
 - % Identity 72.7
 - Alignment Length 77
 - Location of Alignment in SEQ ID NO 2516: from 75 to 151
 - Alignment No. 15298
 - gi No. 4902879
 - % Identity 72.7
 - Alignment Length 44
 - Location of Alignment in SEQ ID NO 2516: from 36 to 79
 - (B) Polypeptide Sequence
 - Pat. Appln. SEQ ID NO 2517
 - Ceres seq_id 1503706
 - Location of start within SEQ ID NO 2514: at 72 nt.
- (C) Nomination and Annotation of Domains within Predicted Polypeptide(s) $% \left(1\right) =\left(1\right) \left(1\right) +\left(1\right) \left(1\right) \left(1\right) +\left(1\right) \left(1\right)$
 - (D) Related Amino Acid Sequences
 - Alignment No. 15299
 - gi No. 4512664
 - % Identity 77.8
 - Alignment Length 45
 - Location of Alignment in SEQ ID NO 2517: from 12 to 56
 - Alignment No. 15300
 - gi No. 4874278
 - % Identity 74
 - Alignment Length 77
 - Location of Alignment in SEQ ID NO 2517: from 52 to 128
 - Alignment No. 15301
 - gi No. 4902470
 - % Identity 74

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- Alignment Length 77
- Location of Alignment in SEQ ID NO 2517: from 52 to 128
- Alignment No. 15302
- gi No. 4902877
- % Identity 72.7
- Alignment Length 77
- Location of Alignment in SEQ ID NO 2517: from 52 to 128
- Alignment No. 15303
- gi No. 4902879
- % Identity 72.7
- Alignment Length 44
- Location of Alignment in SEQ ID NO 2517: from 13 to 56

- (A) Polynucleotide Sequence
 - Pat. Appln. SEQ ID NO 2518
 - Ceres seq_id 1503714
 - (B) Polypeptide Sequence
 - Pat. Appln. SEQ ID NO 2519
 - Ceres seq id 1503715
 - Location of start within SEQ ID NO 2518: at 1 nt.
- - Alignment No. 15304
 - 7 transmembrane receptor (rhodopsin family)
 - Location within SEQ ID NO 2519: from 36 to 129 aa.
 - (D) Related Amino Acid Sequences
 - Alignment No. 15305
 - gi No. 141279
 - % Identity 70.6
 - Alignment Length 17
 - Location of Alignment in SEQ ID NO 2519: from 46 to 62
 - Alignment No. 15306
 - gi No. 1914851
 - % Identity 70.6
 - Alignment Length 17
 - Location of Alignment in SEQ ID NO 2519: from 46 to 61
 - Alignment No. 15307
 - gi No. 2224619
 - % Identity 70
 - Alignment Length 22
 - Location of Alignment in SEQ ID NO 2519: from 49 to 68
 - Alignment No. 15308
 - gi No. 539033
 - % Identity 72
 - Alignment Length 26
 - Location of Alignment in SEQ ID NO 2519: from 46 to 70
 - Alignment No. 15309
 - gi No. 688080
 - % Identity 71.4
 - Alignment Length 14
 - Location of Alignment in SEQ ID NO 2519: from 48 to 60

- (B) Polypeptide Sequence
 - Pat. Appln. SEQ ID NO 2520
 - Ceres seq_id 1503716
 - Location of start within SEQ ID NO 2518: at 2 nt.
- (C) Nomination and Annotation of Domains within Predicted Polypeptide(s)
 - (D) Related Amino Acid Sequences
 - (B) Polypeptide Sequence
 - Pat. Appln. SEQ ID NO 2521
 - Ceres seq_id 1503717
 - Location of start within SEQ ID NO 2518: at 65 nt.
- (C) Nomination and Annotation of Domains within Predicted Polypeptide(s)
 - (D) Related Amino Acid Sequences

- (A) Polynucleotide Sequence
 - Pat. Appln. SEQ ID NO 2522
 - Ceres seq_id 1503718
 - (B) Polypeptide Sequence
 - Pat. Appln. SEQ ID NO 2523
 - Ceres seq_id 1503719
 - Location of start within SEQ ID NO 2522: at 3 nt.
- - Alignment No. 15310
 - Cystatin domain
 - Location within SEQ ID NO 2523: from 77 to 132 aa.
 - (D) Related Amino Acid Sequences

- (A) Polynucleotide Sequence
 - Pat. Appln. SEQ ID NO 2524
 - Ceres seq_id 1503720
 - (B) Polypeptide Sequence
 - Pat. Appln. SEQ ID NO 2525
 - Ceres seq_id 1503721
 - Location of start within SEQ ID NO 2524: at 3 nt.
- - (D) Related Amino Acid Sequences
 - (B) Polypeptide Sequence
 - Pat. Appln. SEQ ID NO 2526
 - Ceres seq_id 1503722
 - Location of start within SEQ ID NO 2524: at 49 nt.
- - (D) Related Amino Acid Sequences
 - (B) Polypeptide Sequence
 - Pat. Appln. SEQ ID NO 2527
 - Ceres seq id 1503723
 - Location of start within SEQ ID NO 2524: at 200 nt.

- - Alignment No. 15311
 - Armadillo/beta-catenin-like repeats
 - Location within SEQ ID NO 2527: from 21 to 62 aa.
 - (D) Related Amino Acid Sequences
 - Alignment No. 15312
 - gi No. 2950210
 - % Identity 73
 - Alignment Length 74
 - Location of Alignment in SEQ ID NO 2527: from 21 to 93
 - Alignment No. 15313
 - gi No. 3091280
 - % Identity 70.2
 - Alignment Length 57
 - Location of Alignment in SEQ ID NO 2527: from 22 to 77
 - Alignment No. 15314
 - gi No. 3122278
 - % Identity 71.9
 - Alignment Length 57
 - Location of Alignment in SEQ ID NO 2527: from 22 to 77
 - Alignment No. 15315
 - gi No. 3273243
 - % Identity 71.6
 - Alignment Length 74
 - Location of Alignment in SEQ ID NO 2527: from 21 to 93

- (A) Polynucleotide Sequence
 - Pat. Appln. SEQ ID NO 2528
 - Ceres seq_id 1503728
 - (B) Polypeptide Sequence
 - Pat. Appln. SEQ ID NO 2529
 - Ceres seq_id 1503729
 - Location of start within SEQ ID NO 2528: at 2 nt.
- - Alignment No. 15316
 - Eukaryotic protein kinase domain
 - Location within SEQ ID NO 2529: from 4 to 108 aa.
 - (D) Related Amino Acid Sequences

- (A) Polynucleotide Sequence
 - Pat. Appln. SEQ ID NO 2530
 - Ceres seq_id 1503734
 - (B) Polypeptide Sequence
 - Pat. Appln. SEQ ID NO 2531
 - Ceres seq_id 1503735
 - Location of start within SEQ ID NO 2530: at 1 nt.
- - Alignment No. 15317

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- Multicopper oxidase
- Location within SEQ ID NO 2531: from 22 to 84 aa.
- (D) Related Amino Acid Sequences
 - Alignment No. 15318
 - gi No. 4454012
 - % Identity 71.6
 - Alignment Length 88
 - Location of Alignment in SEQ ID NO 2531: from 23 to 110
 - Alignment No. 15319
 - gi No. 4725941
 - % Identity 71.9
 - Alignment Length 89
 - Location of Alignment in SEQ ID NO 2531: from 22 to 110
- (B) Polypeptide Sequence
 - Pat. Appln. SEQ ID NO 2532
 - Ceres seq id 1503736
 - Location of start within SEQ ID NO 2530: at 3 nt.
- (C) Nomination and Annotation of Domains within Predicted Polypeptide(s)
 - (D) Related Amino Acid Sequences
 - (B) Polypeptide Sequence
 - Pat. Appln. SEQ ID NO 2533
 - Ceres seq_id 1503737
 - Location of start within SEQ ID NO 2530: at 49 nt.
- (C) Nomination and Annotation of Domains within Predicted Polypeptide(s) $\label{eq:continuous}$
 - Alignment No. 15320
 - Multicopper oxidase
 - Location within SEQ ID NO 2533: from 6 to 68 aa.
 - (D) Related Amino Acid Sequences
 - Alignment No. 15321
 - gi No. 4454012
 - % Identity 71.6
 - Alignment Length 88
 - Location of Alignment in SEQ ID NO 2533: from 7 to 94
 - Alignment No. 15322
 - qi No. 4725941
 - % Identity 71.9
 - Alignment Length 89
 - Location of Alignment in SEQ ID NO 2533: from 6 to 94

- (A) Polynucleotide Sequence
 - Pat. Appln. SEQ ID NO 2534
 - Ceres seq_id 1503743
 - (B) Polypeptide Sequence
 - Pat. Appln. SEQ ID NO 2535
 - Ceres seg id 1503744
 - Location of start within SEQ ID NO 2534: at 2 nt.
- (C) Nomination and Annotation of Domains within Predicted Polypeptide(s)
 - (D) Related Amino Acid Sequences

- (B) Polypeptide Sequence
 - Pat. Appln. SEQ ID NO 2536
 - Ceres seq_id 1503745
 - Location of start within SEQ ID NO 2534: at 3 nt.
- - (D) Related Amino Acid Sequences
 - Alignment No. 15323
 - gi No. 1076556
 - % Identity 75
 - Alignment Length 12
 - Location of Alignment in SEQ ID NO 2536: from 20 to 31
 - Alignment No. 15324
 - qi No. 1655699
 - % Identity 75
 - Alignment Length 12
 - Location of Alignment in SEQ ID NO 2536: from 18 to 29
 - Alignment No. 15325
 - gi No. 1655699
 - % Identity 75
 - Alignment Length 16
 - Location of Alignment in SEQ ID NO 2536: from 17 to 32
 - Alignment No. 15326
 - gi No. 1655699
 - % Identity 75
 - Alignment Length 16
 - Location of Alignment in SEQ ID NO 2536: from 17 to 32 $\,$
 - Alignment No. 15327
 - gi No. 1655699
 - % Identity 75
 - Alignment Length 16
 - Location of Alignment in SEQ ID NO 2536: from 17 to 32
 - Alignment No. 15328
 - gi No. 1655699
 - % Identity 75
 - Alignment Length 16
 - Location of Alignment in SEQ ID NO 2536: from 17 to 32
 - Alignment No. 15329
 - gi No. 1655699
 - % Identity 75
 - Alignment Length 16
 - Location of Alignment in SEQ ID NO 2536: from 17 to 32
 - Alignment No. 15330
 - gi No. 1655699
 - % Identity 70.6
 - Alignment Length 17
 - Location of Alignment in SEQ ID NO 2536: from 17 to 32
 - Alignment No. 15331
 - gi No. 1655699
 - % Identity 70.6
 - Alignment Length 17

- Location of Alignment in SEQ ID NO 2536: from 17 to 32
- Alignment No. 15332
- gi No. 322747
- % Identity 72.2
- Alignment Length 18
- Location of Alignment in SEQ ID NO 2536: from 17 to 30
- Alignment No. 15333
- gi No. 322749
- % Identity 72.2
- Alignment Length 18
- Location of Alignment in SEQ ID NO 2536: from 17 to 30

- (A) Polynucleotide Sequence
 - Pat. Appln. SEQ ID NO 2537
 - Ceres seq_id 1503746
 - (B) Polypeptide Sequence
 - Pat. Appln. SEQ ID NO 2538
 - Ceres seq_id 1503747
 - Location of start within SEQ ID NO 2537: at 1 nt.
- (C) Nomination and Annotation of Domains within Predicted Polypeptide(s)
 - (D) Related Amino Acid Sequences
 - (B) Polypeptide Sequence
 - Pat. Appln. SEQ ID NO 2539
 - Ceres seq_id 1503748
 - Location of start within SEQ ID NO 2537: at 68 nt.
- (C) Nomination and Annotation of Domains within Predicted Polypeptide(s)
 - (D) Related Amino Acid Sequences
 - Alignment No. 15334
 - gi No. 112110
 - % Identity 74.1
 - Alignment Length 27
 - Location of Alignment in SEQ ID NO 2539: from 2 to 28
 - (B) Polypeptide Sequence
 - Pat. Appln. SEQ ID NO 2540
 - Ceres seq_id 1503749
 - Location of start within SEQ ID NO 2537: at 301 nt.
- (C) Nomination and Annotation of Domains within Predicted Polypeptide(s) $\label{eq:continuous}$
 - (D) Related Amino Acid Sequences

- (A) Polynucleotide Sequence
 - Pat. Appln. SEQ ID NO 2541
 - Ceres seq_id 1503769
 - (B) Polypeptide Sequence
 - Pat. Appln. SEQ ID NO 2542
 - Ceres seq_id 1503770
 - Location of start within SEQ ID NO 2541: at 104 nt.
- (C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 15335
- Nucleoside diphosphate kinases
- Location within SEQ ID NO 2542: from 2 to 114 aa.
- (D) Related Amino Acid Sequences
 - Alignment No. 15336
 - gi No. 1076713
 - % Identity 87
 - Alignment Length 23
 - Location of Alignment in SEQ ID NO 2542: from 1 to 22
 - Alignment No. 15337
 - gi No. 1304478
 - % Identity 73
 - Alignment Length 37
 - Location of Alignment in SEQ ID NO 2542: from 2 to 38
 - Alignment No. 15338
 - qi No. 1729427
 - % Identity 71.1
 - Alignment Length 38
 - Location of Alignment in SEQ ID NO 2542: from 1 to 38
 - Alignment No. 15339
 - gi No. 2129487
 - % Identity 80.2
 - Alignment Length 116
 - Location of Alignment in SEQ ID NO 2542: from 1 to 114
 - Alignment No. 15340
 - gi No. 2829275
 - % Identity 88.8
 - Alignment Length 116
 - Location of Alignment in SEQ ID NO 2542: from 1 to 114
 - Alignment No. 15341
 - gi No. 4972094
 - % Identity 90.5
 - Alignment Length 116
 - Location of Alignment in SEQ ID NO 2542: from 1 to 114

- (A) Polynucleotide Sequence
 - Pat. Appln. SEQ ID NO 2543
 - Ceres seq_id 1503775
 - (B) Polypeptide Sequence
 - Pat. Appln. SEQ ID NO 2544
 - Ceres seq_id 1503776
 - Location of start within SEQ ID NO 2543: at 2 nt.
- - Alignment No. 15342
 - Elongation factor G C-terminus
 - Location within SEQ ID NO 2544: from 21 to 152 aa.
 - (D) Related Amino Acid Sequences
 - Alignment No. 15343
 - gi No. 4895248
 - % Identity 83.3
 - Alignment Length 156



- Location of Alignment in SEQ ID NO 2544: from 1 to 156
- (B) Polypeptide Sequence
 - Pat. Appln. SEQ ID NO 2545
 - Ceres seq id 1503777
 - Location of start within SEQ ID NO 2543: at 110 nt.
- - Alignment No. 15344
 - Elongation factor G C-terminus
 - Location within SEQ ID NO 2545: from 1 to 116 aa.
 - (D) Related Amino Acid Sequences
 - Alignment No. 15345
 - gi No. 4895248
 - % Identity 83.3
 - Alignment Length 156
 - Location of Alignment in SEQ ID NO 2545: from 1 to 120

- (A) Polynucleotide Sequence
 - Pat. Appln. SEQ ID NO 2546
 - Ceres seq id 1503778
 - (B) Polypeptide Sequence
 - Pat. Appln. SEQ ID NO 2547
 - Ceres seq_id 1503779
 - Location of start within SEQ ID NO 2546: at 3 nt.
- - (D) Related Amino Acid Sequences
 - Alignment No. 15346
 - gi No. 3786005
 - % Identity 80.8
 - Alignment Length 26
 - Location of Alignment in SEQ ID NO 2547: from 1 to 26
 - (B) Polypeptide Sequence
 - Pat. Appln. SEQ ID NO 2548
 - Ceres seq id 1503780
 - Location of start within SEQ ID NO 2546: at 269 nt.
- (C) Nomination and Annotation of Domains within Predicted Polypeptide(s)
 - (D) Related Amino Acid Sequences
 - (B) Polypeptide Sequence
 - Pat. Appln. SEQ ID NO 2549
 - Ceres seq_id 1503781
 - Location of start within SEQ ID NO 2546: at 324 nt.
- - (D) Related Amino Acid Sequences

- (A) Polynucleotide Sequence
 - Pat. Appln. SEQ ID NO 2550
 - Ceres seq_id 1503796
 - (B) Polypeptide Sequence

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- Pat. Appln. SEQ ID NO 2551
- Ceres seq_id 1503797
- Location of start within SEQ ID NO 2550: at 2 nt.
- (C) Nomination and Annotation of Domains within Predicted Polypeptide(s)
 - (D) Related Amino Acid Sequences
 - (B) Polypeptide Sequence
 - Pat. Appln. SEQ ID NO 2552
 - Ceres seq_id 1503798
 - Location of start within SEQ ID NO 2550: at 153 nt.
- (C) Nomination and Annotation of Domains within Predicted Polypeptide(s)
 - (D) Related Amino Acid Sequences
 - Alignment No. 15347
 - qi No. 2352921
 - % Identity 87.1
 - Alignment Length 62
 - Location of Alignment in SEQ ID NO 2552: from 1 to 38
 - Alignment No. 15348
 - gi No. 2352923
 - % Identity 82.3
 - Alignment Length 62
 - Location of Alignment in SEQ ID NO 2552: from 1 to 38
 - Alignment No. 15349
 - gi No. 3021508
 - % Identity 73.1
 - Alignment Length 67
 - Location of Alignment in SEQ ID NO 2552: from 1 to 41
 - Alignment No. 15350
 - gi No. 3021510
 - % Identity 76.1
 - Alignment Length 67
 - Location of Alignment in SEQ ID NO 2552: from 1 to 41
 - Alignment No. 15351
 - gi No. 3023815
 - % Identity 77.4
 - Alignment Length 62
 - Location of Alignment in SEQ ID NO 2552: from 1 to 38
 - Alignment No. 15352
 - gi No. 4206114
 - % Identity 77.6
 - Alignment Length 67
 - Location of Alignment in SEQ ID NO 2552: from 1 to 41
 - Alignment No. 15353
 - qi No. 5360754
 - % Identity 87.5
 - Alignment Length 56
 - Location of Alignment in SEQ ID NO 2552: from 1 to 41
 - Alignment No. 15354
 - gi No. 585165
 - % Identity 76.1

- Alignment Length 67
- Location of Alignment in SEQ ID NO 2552: from 1 to 41
- (B) Polypeptide Sequence
 - Pat. Appln. SEQ ID NO 2553
 - Ceres seq_id 1503799
 - Location of start within SEQ ID NO 2550: at 262 nt.
- (C) Nomination and Annotation of Domains within Predicted Polypeptide(s)
 - Alignment No. 15355
 - Glucose-6-phosphate dehydrogenase
 - Location within SEQ ID NO 2553: from 1 to 42 aa.
 - (D) Related Amino Acid Sequences
 - Alignment No. 15356
 - gi No. 1169799
 - % Identity 70.7
 - Alignment Length 41
 - Location of Alignment in SEQ ID NO 2553: from 3 to 43
 - Alignment No. 15357
 - qi No. 3021508
 - % Identity 81
 - Alignment Length 42
 - Location of Alignment in SEQ ID NO 2553: from 3 to 43
 - Alignment No. 15358
 - gi No. 585165
 - % Identity 75
 - Alignment Length 48
 - Location of Alignment in SEQ ID NO 2553: from 1 to 43

- (A) Polynucleotide Sequence
 - Pat. Appln. SEQ ID NO 2554
 - Ceres seq_id 1503810
 - (B) Polypeptide Sequence
 - Pat. Appln. SEQ ID NO 2555
 - Ceres seq_id 1503811
 - Location of start within SEQ ID NO 2554: at 3 nt.
- (C) Nomination and Annotation of Domains within Predicted Polypeptide(s)
 - (D) Related Amino Acid Sequences
 - Alignment No. 15359
 - gi No. 1173201
 - % Identity 75.7
 - Alignment Length 37
 - Location of Alignment in SEQ ID NO 2555: from 37 to 73 $\,$
 - Alignment No. 15360
 - gi No. 131772
 - % Identity 97.6
 - Alignment Length 41
 - Location of Alignment in SEQ ID NO 2555: from 33 to 73
 - Alignment No. 15361
 - gi No. 131773
 - % Identity 89.7
 - Alignment Length 39



- Location of Alignment in SEQ ID NO 2555: from 35 to 73
- Alignment No. 15362
- gi No. 133720
- % Identity 71.4
- Alignment Length 14
- Location of Alignment in SEQ ID NO 2555: from 60 to 73
- Alignment No. 15363
- gi No. 2350992
- % Identity 80
- Alignment Length 15
- Location of Alignment in SEQ ID NO 2555: from 59 to 73
- Alignment No. 15364
- gi No. 2414647
- % Identity 76.9
- Alignment Length 26
- Location of Alignment in SEQ ID NO 2555: from 48 to 73
- Alignment No. 15365
- gi No. 3097244
- % Identity 71.4
- Alignment Length 42
- Location of Alignment in SEQ ID NO 2555: from 33 to 73
- Alignment No. 15366
- gi No. 3122785
- % Identity 78
- Alignment Length 41
- Location of Alignment in SEQ ID NO 2555: from 33 to 73
- Alignment No. 15367
- gi No. 4574240
- % Identity 76.2
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2555: from 53 to 73
- Alignment No. 15368
- gi No. 4678226
- % Identity 80.5
- Alignment Length 41
- Location of Alignment in SEQ ID NO 2555: from 33 to 73
- Alignment No. 15369
- gi No. 4886269
- % Identity 82.9
- Alignment Length 41
- Location of Alignment in SEQ ID NO 2555: from 33 to 73
- (B) Polypeptide Sequence
 - Pat. Appln. SEQ ID NO 2556
 - Ceres seq_id 1503812
 - Location of start within SEQ ID NO 2554: at 99 nt.
- (C) Nomination and Annotation of Domains within Predicted Polypeptide(s)
 - (D) Related Amino Acid Sequences
 - Alignment No. 15370
 - gi No. 1173201
 - % Identity 75.7

- Alignment Length 37
- Location of Alignment in SEQ ID NO 2556: from 5 to 41
- Alignment No. 15371
- gi No. 131772
- % Identity 97.6
- Alignment Length 41
- Location of Alignment in SEQ ID NO 2556: from 1 to 41
- Alignment No. 15372
- gi No. 131773
- % Identity 89.7
- Alignment Length 39
- Location of Alignment in SEQ ID NO 2556: from 3 to 41
- Alignment No. 15373
- gi No. 133720
- % Identity 71.4
- Alignment Length 14
- Location of Alignment in SEQ ID NO 2556: from 28 to 41
- Alignment No. 15374
- gi No. 2350992
- % Identity 80
- Alignment Length 15
- Location of Alignment in SEQ ID NO 2556: from 27 to 41
- Alignment No. 15375
- gi No. 2414647
- % Identity 76.9
- Alignment Length 26
- Location of Alignment in SEQ ID NO 2556: from 16 to 41
- Alignment No. 15376
- gi No. 3097244
- % Identity 71.4
- Alignment Length 42
- Location of Alignment in SEQ ID NO 2556: from 1 to 41
- Alignment No. 15377
- gi No. 3122785
- % Identity 78
- Alignment Length 41
- Location of Alignment in SEQ ID NO 2556: from 1 to 41
- Alignment No. 15378
- gi No. 4574240
- % Identity 76.2
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2556: from 21 to 41
- Alignment No. 15379
- gi No. 4678226
- % Identity 80.5
- Alignment Length 41
- Location of Alignment in SEQ ID NO 2556: from 1 to 41
- Alignment No. 15380
- gi No. 4886269
- % Identity 82.9
- Alignment Length 41

- Location of Alignment in SEQ ID NO 2556: from 1 to 41
- (B) Polypeptide Sequence
 - Pat. Appln. SEQ ID NO 2557
 - Ceres seq_id 1503813
 - Location of start within SEQ ID NO 2554: at 295 nt.
- - Alignment No. 15381
 - Ribosomal protein S11
 - Location within SEQ ID NO 2557: from 3 to 68 aa.
 - (D) Related Amino Acid Sequences
 - Alignment No. 15382
 - gi No. 1173200
 - % Identity 90.2
 - Alignment Length 41
 - Location of Alignment in SEQ ID NO 2557: from 28 to 68
 - Alignment No. 15383
 - gi No. 1173201
 - % Identity 89.4
 - Alignment Length 66
 - Location of Alignment in SEQ ID NO 2557: from 3 to 68
 - Alignment No. 15384
 - gi No. 131772
 - % Identity 97
 - Alignment Length 66
 - Location of Alignment in SEQ ID NO 2557: from 3 to 68
 - Alignment No. 15385
 - gi No. 131773
 - % Identity 95.5
 - Alignment Length 66
 - Location of Alignment in SEQ ID NO 2557: from 3 to 68
 - Alignment No. 15386
 - gi No. 133771
 - % Identity 86.4
 - Alignment Length 66
 - Location of Alignment in SEQ ID NO 2557: from 3 to 68
 - Alignment No. 15387
 - gi No. 133777
 - % Identity 80.3
 - Alignment Length 66
 - Location of Alignment in SEQ ID NO 2557: from 3 to 68
 - Alignment No. 15388
 - gi No. 133782
 - % Identity 82.4
 - Alignment Length 68
 - Location of Alignment in SEQ ID NO 2557: from 3 to 68
 - Alignment No. 15389
 - gi No. 133785
 - % Identity 89.4
 - Alignment Length 66
 - Location of Alignment in SEQ ID NO 2557: from 3 to 68

- Alignment No. 15390 - gi No. 133789 - % Identity 75.8 - Alignment Length 66 - Location of Alignment in SEQ ID NO 2557: from 3 to 68 - Alignment No. 15391 - gi No. 1346941 - % Identity 77.3 - Alignment Length 66 - Location of Alignment in SEQ ID NO 2557: from 3 to 68 - Alignment No. 15392 - gi No. 1350935 - % Identity 83.3 - Alignment Length 66 - Location of Alignment in SEQ ID NO 2557: from 3 to 68 - Alignment No. 15393 - gi No. 1350937 - % Identity 84.8 - Alignment Length 66 - Location of Alignment in SEQ ID NO 2557: from 3 to 68 - Alignment No. 15394 - gi No. 2350992 - % Identity 72.1 - Alignment Length 68 - Location of Alignment in SEQ ID NO 2557: from 3 to 69 - Alignment No. 15395 - gi No. 2414647 - % Identity 77.3 - Alignment Length 66 - Location of Alignment in SEQ ID NO 2557: from 3 to 68 - Alignment No. 15396 - gi No. 2500442 - % Identity 74.4 - Alignment Length 39 - Location of Alignment in SEQ ID NO 2557: from 3 to 41 - Alignment No. 15397 - gi No. 2500443 - % Identity 87 - Alignment Length 23 - Location of Alignment in SEQ ID NO 2557: from 46 to 68 - Alignment No. 15398 - gi No. 3097244 - % Identity 89.4 - Alignment Length 66
- Alignment No. 15399
- gi No. 3122785
- % Identity 95.5
- Alignment Length 66
- Location of Alignment in SEQ ID NO 2557: from 3 to 68

- Location of Alignment in SEQ ID NO 2557: from 3 to 68

- Alignment No. 15400
- gi No. 4574240
- % Identity 84.8
- Alignment Length 66
- Location of Alignment in SEQ ID NO 2557: from 3 to 68
- Alignment No. 15401
- gi No. 4588920
- % Identity 86.4
- Alignment Length 66
- Location of Alignment in SEQ ID NO 2557: from 3 to 68
- Alignment No. 15402
- gi No. 4678226
- % Identity 93.9
- Alignment Length 66
- Location of Alignment in SEQ ID NO 2557: from 3 to 68
- Alignment No. 15403
- gi No. 4886269
- % Identity 93.9
- Alignment Length 66
- Location of Alignment in SEQ ID NO 2557: from 3 to 68
- Alignment No. 15404
- gi No. 5032051
- % Identity 89.4
- Alignment Length 66
- Location of Alignment in SEQ ID NO 2557: from 3 to 68
- Alignment No. 15405
- gi No. 5441523
- % Identity 91.7
- Alignment Length 36
- Location of Alignment in SEQ ID NO 2557: from 33 to 68
- Alignment No. 15406
- gi No. 547604
- % Identity 78.8
- Alignment Length 66
- Location of Alignment in SEQ ID NO 2557: from 3 to 68
- Alignment No. 15407
- gi No. 70946
- % Identity 77.3
- Alignment Length 66
- Location of Alignment in SEQ ID NO 2557: from 3 to 68
- Alignment No. 15408
- gi No. 730453
- % Identity 78.8
- Alignment Length 66
- Location of Alignment in SEQ ID NO 2557: from 3 to 68
- Alignment No. 15409
- gi No. 730633
- % Identity 84.8
- Alignment Length 66
- Location of Alignment in SEQ ID NO 2557: from 3 to 68
- Alignment No. 15410

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- qi No. 83794
- % Identity 84.8
- Alignment Length 66
- Location of Alignment in SEQ ID NO 2557: from 3 to 68

Maximum Length Sequence corresponding to clone ID 315681

- (A) Polynucleotide Sequence
 - Pat. Appln. SEQ ID NO 2558
 - Ceres seq_id 1503822
 - (B) Polypeptide Sequence
 - Pat. Appln. SEQ ID NO 2559
 - Ceres seq id 1503823
 - Location of start within SEQ ID NO 2558: at 3 nt.
- - Alignment No. 15411
 - 6,7-dimethyl-8-ribityllumazine synthase
 - Location within SEQ ID NO 2559: from 57 to 150 aa.
 - (D) Related Amino Acid Sequences
 - (B) Polypeptide Sequence
 - Pat. Appln. SEQ ID NO 2560
 - Ceres seq_id 1503824
 - Location of start within SEQ ID NO 2558: at 84 nt.
- (C) Nomination and Annotation of Domains within Predicted Polypeptide(s)
 - Alignment No. 15412
 - 6,7-dimethyl-8-ribityllumazine synthase
 - Location within SEQ ID NO 2560: from 30 to 123 aa.
 - (D) Related Amino Acid Sequences
 - (B) Polypeptide Sequence
 - Pat. Appln. SEQ ID NO 2561
 - Ceres seq_id 1503825
 - Location of start within SEQ ID NO 2558: at 150 nt.
- (C) Nomination and Annotation of Domains within Predicted Polypeptide(s)
 - Alignment No. 15413
 - 6,7-dimethyl-8-ribityllumazine synthase
 - Location within SEQ ID NO 2561: from 8 to 101 aa.
 - (D) Related Amino Acid Sequences

- (A) Polynucleotide Sequence
 - Pat. Appln. SEQ ID NO 2562
 - Ceres seq_id 1503826
 - (B) Polypeptide Sequence
 - Pat. Appln. SEQ ID NO 2563
 - Ceres seq id 1503827
 - Location of start within SEQ ID NO 2562: at 1 nt.
- (C) Nomination and Annotation of Domains within Predicted Polypeptide(s)
 - (D) Related Amino Acid Sequences
 - Alignment No. 15414

- gi No. 1834333
- % Identity 89.5
- Alignment Length 19
- Location of Alignment in SEQ ID NO 2563: from 99 to 117
- (B) Polypeptide Sequence
 - Pat. Appln. SEQ ID NO 2564
 - Ceres seq_id 1503828
 - Location of start within SEQ ID NO 2562: at 22 nt.
- (C) Nomination and Annotation of Domains within Predicted Polypeptide(s)
 - (D) Related Amino Acid Sequences
 - Alignment No. 15415
 - gi No. 1834333
 - % Identity 89.5
 - Alignment Length 19
 - Location of Alignment in SEQ ID NO 2564: from 92 to 110
 - (B) Polypeptide Sequence
 - Pat. Appln. SEQ ID NO 2565
 - Ceres seq_id 1503829
 - Location of start within SEQ ID NO 2562: at 61 nt.
- - (D) Related Amino Acid Sequences
 - Alignment No. 15416
 - gi No. 1834333
 - % Identity 89.5
 - Alignment Length 19
 - Location of Alignment in SEQ ID NO 2565: from 79 to 97

- (A) Polynucleotide Sequence
 - Pat. Appln. SEQ ID NO 2566
 - Ceres seq_id 1503869
 - (B) Polypeptide Sequence
 - Pat. Appln. SEQ ID NO 2567
 - Ceres seq_id 1503870
 - Location of start within SEQ ID NO 2566: at 3 nt.
- - (D) Related Amino Acid Sequences
 - (B) Polypeptide Sequence
 - Pat. Appln. SEQ ID NO 2568
 - Ceres seq_id 1503871
 - Location of start within SEQ ID NO 2566: at 219 nt.
- (C) Nomination and Annotation of Domains within Predicted Polypeptide(s)
 - (D) Related Amino Acid Sequences
 - Alignment No. 15417
 - gi No. 2072023
 - % Identity 82.3
 - Alignment Length 79
 - Location of Alignment in SEQ ID NO 2568: from 3 to 81
 - Alignment No. 15418

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- gi No. 2245008
- % Identity 91.2
- Alignment Length 68
- Location of Alignment in SEQ ID NO 2568: from 14 to 81
- Alignment No. 15419
- gi No. 2583137
- % Identity 88
- Alignment Length 50
- Location of Alignment in SEQ ID NO 2568: from 32 to 81
- Alignment No. 15420
- gi No. 2961343
- % Identity 87.9
- Alignment Length 66
- Location of Alignment in SEQ ID NO 2568: from 17 to 81
- Alignment No. 15421
- gi No. 3024687
- % Identity 82.3
- Alignment Length 79
- Location of Alignment in SEQ ID NO 2568: from 3 to 81
- Alignment No. 15422
- gi No. 3367536
- % Identity 78.5
- Alignment Length 93
- Location of Alignment in SEQ ID NO 2568: from 1 to 81
- Alignment No. 15423
- gi No. 3810848
- % Identity 74.7
- Alignment Length 79
- Location of Alignment in SEQ ID NO 2568: from 3 to 81
- Alignment No. 15424
- gi No. 4581162
- % Identity 87.8
- Alignment Length 82
- Location of Alignment in SEQ ID NO 2568: from 1 to 81
- Alignment No. 15425
- qi No. 4773906
- % Identity 76.8
- Alignment Length 82
- Location of Alignment in SEQ ID NO 2568: from 1 to 81
- Alignment No. 15426
- gi No. 4895235
- % Identity 82.1
- Alignment Length 78
- Location of Alignment in SEQ ID NO 2568: from 4 to 81
- Alignment No. 15427
- gi No. 586441
- % Identity 72.2
- Alignment Length 79
- Location of Alignment in SEQ ID NO 2568: from 3 to 81
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Maximum Length Sequence corresponding to clone ID 315827 (A) Polynucleotide Sequence

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- Pat. Appln. SEQ ID NO 2569
- Ceres seq_id 1503873
- (B) Polypeptide Sequence
 - Pat. Appln. SEQ ID NO 2570
 - Ceres seq_id 1503874
 - Location of start within SEQ ID NO 2569: at 2 nt.
- (C) Nomination and Annotation of Domains within Predicted Polypeptide(s)
 - (D) Related Amino Acid Sequences
 - (B) Polypeptide Sequence
 - Pat. Appln. SEQ ID NO 2571
 - Ceres seq id 1503875
 - Location of start within SEQ ID NO 2569: at 8 nt.
- (C) Nomination and Annotation of Domains within Predicted Polypeptide(s)
 - (D) Related Amino Acid Sequences
 - (B) Polypeptide Sequence
 - Pat. Appln. SEQ ID NO 2572
 - Ceres seq id 1503876
 - Location of start within SEQ ID NO 2569: at 58 nt.
- (C) Nomination and Annotation of Domains within Predicted Polypeptide(s)
 - (D) Related Amino Acid Sequences
 - Alignment No. 15428
 - gi No. 4539333
 - % Identity 71.4
 - Alignment Length 14
 - Location of Alignment in SEQ ID NO 2572: from 52 to 65

- (A) Polynucleotide Sequence
 - Pat. Appln. SEQ ID NO 2573
 - Ceres seq_id 1503886
 - (B) Polypeptide Sequence
 - Pat. Appln. SEQ ID NO 2574
 - Ceres seq_id 1503887
 - Location of start within SEQ ID NO 2573: at 1 nt.
- (C) Nomination and Annotation of Domains within Predicted Polypeptide(s)
 - (D) Related Amino Acid Sequences
 - (B) Polypeptide Sequence
 - Pat. Appln. SEQ ID NO 2575
 - Ceres seq_id 1503888
 - Location of start within SEQ ID NO 2573: at 2 nt.
- - (D) Related Amino Acid Sequences
 - (B) Polypeptide Sequence
 - Pat. Appln. SEQ ID NO 2576
 - Ceres seq_id 1503889
 - Location of start within SEQ ID NO 2573: at 3 nt.

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- (C) Nomination and Annotation of Domains within Predicted Polypeptide(s)
 - (D) Related Amino Acid Sequences
 - Alignment No. 15429
 - qi No. 3387886
 - % Identity 83.3
 - Alignment Length 12
 - Location of Alignment in SEQ ID NO 2576: from 1 to 12
 - Alignment No. 15430
 - gi No. 3402680
 - % Identity 75
 - Alignment Length 12
 - Location of Alignment in SEQ ID NO 2576: from 3 to 14

- (A) Polynucleotide Sequence
 - Pat. Appln. SEQ ID NO 2577
 - Ceres seq id 1503890
 - (B) Polypeptide Sequence
 - Pat. Appln. SEQ ID NO 2578
 - Ceres seq id 1503891
 - Location of start within SEQ ID NO 2577: at 1 nt.
- (C) Nomination and Annotation of Domains within Predicted Polypeptide(s)
 - Alignment No. 15431
 - Peroxidase
 - Location within SEQ ID NO 2578: from 48 to 111 aa.
 - (D) Related Amino Acid Sequences
 - Alignment No. 15432
 - gi No. 1076635
 - % Identity 86.7
 - Alignment Length 15
 - Location of Alignment in SEQ ID NO 2578: from 68 to 82
 - Alignment No. 15433
 - gi No. 5002334
 - % Identity 73.7
 - Alignment Length 38
 - Location of Alignment in SEQ ID NO 2578: from 74 to 111
 - (B) Polypeptide Sequence
 - Pat. Appln. SEQ ID NO 2579
 - Ceres seq_id 1503892
 - Location of start within SEQ ID NO 2577: at 3 nt.
- (C) Nomination and Annotation of Domains within Predicted Polypeptide(s)
 - (D) Related Amino Acid Sequences
 - (B) Polypeptide Sequence
 - Pat. Appln. SEQ ID NO 2580
 - Ceres seq_id 1503893
 - Location of start within SEQ ID NO 2577: at 22 nt.
- (C) Nomination and Annotation of Domains within Predicted Polypeptide(s)
 - Alignment No. 15434
 - Peroxidase

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(D) Related Amino Acid Sequences
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- Alignment No. 15435
- qi No. 1076635
- % Identity 86.7
- Alignment Length 15
- Location of Alignment in SEQ ID NO 2580: from 61 to 75

- Location within SEQ ID NO 2580: from 41 to 104 aa.

- Alignment No. 15436
- gi No. 5002334
- % Identity 73.7
- Alignment Length 38
- Location of Alignment in SEQ ID NO 2580: from 67 to 104

- (A) Polynucleotide Sequence
 - Pat. Appln. SEQ ID NO 2581
 - Ceres seq_id 1503894
 - (B) Polypeptide Sequence
 - Pat. Appln. SEQ ID NO 2582
 - Ceres seq_id 1503895
 - Location of start within SEQ ID NO 2581: at 2 nt.
- - (D) Related Amino Acid Sequences
 - Alignment No. 15437
 - gi No. 1142653
 - % Identity 74.7
 - Alignment Length 79
 - Location of Alignment in SEQ ID NO 2582: from 79 to 157
 - Alignment No. 15438
 - gi No. 128844
 - % Identity 70.8
 - Alignment Length 24
 - Location of Alignment in SEQ ID NO 2582: from 53 to 76
 - Alignment No. 15439
 - qi No. 4539408
 - % Identity 70.2
 - Alignment Length 125
 - Location of Alignment in SEQ ID NO 2582: from 36 to 159
 - Alignment No. 15440
 - gi No. 5031931
 - % Identity 74.7
 - Alignment Length 79
 - Location of Alignment in SEQ ID NO 2582: from 79 to 157
 - Alignment No. 15441
 - gi No. 92559
 - % Identity 70.8
 - Alignment Length 24
 - Location of Alignment in SEQ ID NO 2582: from 53 to 76
 - (B) Polypeptide Sequence
 - Pat. Appln. SEQ ID NO 2583
 - Ceres seq_id 1503896
 - Location of start within SEQ ID NO 2581: at 68 nt.

- (C) Nomination and Annotation of Domains within Predicted Polypeptide(s)
 - (D) Related Amino Acid Sequences
 - Alignment No. 15442
 - gi No. 1142653
 - % Identity 74.7
 - Alignment Length 79
 - Location of Alignment in SEQ ID NO 2583: from 57 to 135
 - Alignment No. 15443
 - gi No. 128844
 - % Identity 70.8
 - Alignment Length 24
 - Location of Alignment in SEQ ID NO 2583: from 31 to 54
 - Alignment No. 15444
 - gi No. 4539408
 - % Identity 70.2
 - Alignment Length 125
 - Location of Alignment in SEQ ID NO 2583: from 14 to 137
 - Alignment No. 15445
 - gi No. 5031931
 - % Identity 74.7
 - Alignment Length 79
 - Location of Alignment in SEQ ID NO 2583: from 57 to 135
 - Alignment No. 15446
 - gi No. 92559
 - % Identity 70.8
 - Alignment Length 24
 - Location of Alignment in SEQ ID NO 2583: from 31 to 54

- (A) Polynucleotide Sequence
 - Pat. Appln. SEQ ID NO 2584
 - Ceres seq_id 1503899
 - (B) Polypeptide Sequence
 - Pat. Appln. SEQ ID NO 2585
 - Ceres seq_id 1503900
 - Location of start within SEQ ID NO 2584: at 3 nt.
- - Alignment No. 15447
 - Topoisomerase DNA binding C4 zinc finger
 - Location within SEQ ID NO 2585: from 69 to 106 aa.
 - (D) Related Amino Acid Sequences
 - (B) Polypeptide Sequence
 - Pat. Appln. SEQ ID NO 2586
 - Ceres seq_id 1503901
 - Location of start within SEQ ID NO 2584: at 18 nt.
- (C) Nomination and Annotation of Domains within Predicted Polypeptide(s)
 - Alignment No. 15448
 - Topoisomerase DNA binding C4 zinc finger
 - Location within SEQ ID NO 2586: from 64 to 101 aa.

- (D) Related Amino Acid Sequences
- (B) Polypeptide Sequence
 - Pat. Appln. SEQ ID NO 2587
 - Ceres seq_id 1503902
 - Location of start within SEQ ID NO 2584: at 147 nt.
- - Alignment No. 15449
 - Topoisomerase DNA binding C4 zinc finger
 - Location within SEQ ID NO 2587: from 21 to 58 aa.
 - (D) Related Amino Acid Sequences

 ${\tt Maximum\ Length\ Sequence\ corresponding\ to\ clone\ ID\ 316031}$

- (A) Polynucleotide Sequence
 - Pat. Appln. SEQ ID NO 2588
 - Ceres seq_id 1503924
 - (B) Polypeptide Sequence
 - Pat. Appln. SEQ ID NO 2589
 - Ceres seq id 1503925
 - Location of start within SEQ ID NO 2588: at 2 nt.
- - (D) Related Amino Acid Sequences
 - Alignment No. 15450
 - gi No. 3004565
 - % Identity 80
 - Alignment Length 80
 - Location of Alignment in SEQ ID NO 2589: from 1 to 80

- (A) Polynucleotide Sequence
 - Pat. Appln. SEQ ID NO 2590
 - Ceres seq_id 1503926
 - (B) Polypeptide Sequence
 - Pat. Appln. SEQ ID NO 2591
 - Ceres seq id 1503927
 - Location of start within SEQ ID NO 2590: at 2 nt.
- - Alignment No. 15451
 - Protein phosphatase 2C
 - Location within SEQ ID NO 2591: from 24 to 163 aa.
 - (D) Related Amino Acid Sequences
 - Alignment No. 15452
 - gi No. 3927836
 - % Identity 72.7
 - Alignment Length 11
 - Location of Alignment in SEQ ID NO 2591: from 3 to 13
 - (B) Polypeptide Sequence
 - Pat. Appln. SEQ ID NO 2592
 - Ceres seq_id 1503928
 - Location of start within SEQ ID NO 2590: at 17 nt.

- (C) Nomination and Annotation of Domains within Predicted Polypeptide(s)
 - Alignment No. 15453
 - Protein phosphatase 2C
 - Location within SEQ ID NO 2592: from 19 to 158 aa.
 - (D) Related Amino Acid Sequences
 - (B) Polypeptide Sequence
 - Pat. Appln. SEQ ID NO 2593
 - Ceres seq_id 1503929
 - Location of start within SEQ ID NO 2590: at 47 nt.
- - Alignment No. 15454
 - Protein phosphatase 2C
 - Location within SEQ ID NO 2593: from 9 to 148 aa.
 - (D) Related Amino Acid Sequences

- (A) Polynucleotide Sequence
 - Pat. Appln. SEQ ID NO 2594
 - Ceres seq_id 1503934
 - (B) Polypeptide Sequence
 - Pat. Appln. SEQ ID NO 2595
 - Ceres seq_id 1503935
 - Location of start within SEQ ID NO 2594: at 1 nt.
- (C) Nomination and Annotation of Domains within Predicted Polypeptide(s)
 - (D) Related Amino Acid Sequences
 - (B) Polypeptide Sequence
 - Pat. Appln. SEQ ID NO 2596
 - Ceres seq_id 1503936
 - Location of start within SEQ ID NO 2594: at 2 nt.
- - (D) Related Amino Acid Sequences
 - Alignment No. 15455
 - gi No. 3822340
 - % Identity 75
 - Alignment Length 12
 - Location of Alignment in SEQ ID NO 2596: from 37 to 48
 - (B) Polypeptide Sequence
 - Pat. Appln. SEQ ID NO 2597
 - Ceres seq_id 1503937
 - Location of start within SEQ ID NO 2594: at 3 nt.
- (C) Nomination and Annotation of Domains within Predicted Polypeptide(s)
 - (D) Related Amino Acid Sequences

- (A) Polynucleotide Sequence
 - Pat. Appln. SEQ ID NO 2598
 - Ceres seq_id 1503942

- (B) Polypeptide Sequence
 - Pat. Appln. SEQ ID NO 2599
 - Ceres seq id 1503943
 - Location of start within SEQ ID NO 2598: at 1 nt.
- - (D) Related Amino Acid Sequences
 - Alignment No. 15456
 - gi No. 5441235
 - % Identity 72.7
 - Alignment Length 11
 - Location of Alignment in SEQ ID NO 2599: from 74 to 84
 - (B) Polypeptide Sequence
 - Pat. Appln. SEQ ID NO 2600
 - Ceres seq id 1503944
 - Location of start within SEQ ID NO 2598: at 3 nt.
- (C) Nomination and Annotation of Domains within Predicted Polypeptide(s) $\label{eq:condition} % \begin{array}{c} \text{Polyperiod} \\ \text{Poly$
 - Alignment No. 15457
 - Sperm histone P2
 - Location within SEQ ID NO 2600: from 38 to 118 aa.
 - (D) Related Amino Acid Sequences
 - (B) Polypeptide Sequence
 - Pat. Appln. SEQ ID NO 2601
 - Ceres seq id 1503945
 - Location of start within SEQ ID NO 2598: at 124 nt.
- - (D) Related Amino Acid Sequences
 - Alignment No. 15458
 - gi No. 5441235
 - % Identity 72.7
 - Alignment Length 11
 - Location of Alignment in SEQ ID NO 2601: from 33 to 43

- (A) Polynucleotide Sequence
 - Pat. Appln. SEQ ID NO 2602
 - Ceres seq_id 1503946
 - (B) Polypeptide Sequence
 - Pat. Appln. SEQ ID NO 2603
 - Ceres seq_id 1503947
 - Location of start within SEQ ID NO 2602: at 2 nt.
- - Alignment No. 15459
 - Phosphoribosyl pyrophosphate synthetase
 - Location within SEQ ID NO 2603: from 1 to 80 aa.
 - (D) Related Amino Acid Sequences
 - Alignment No. 15460
 - gi No. 2833379
 - % Identity 87.7
 - Alignment Length 81

- Location of Alignment in SEQ ID NO 2603: from 1 to 81
- Alignment No. 15461
- gi No. 2833380
- % Identity 87.7
- Alignment Length 81
- Location of Alignment in SEQ ID NO 2603: from 1 to 81
- Alignment No. 15462
- gi No. 2833468
- % Identity 76.3
- Alignment Length 80
- Location of Alignment in SEQ ID NO 2603: from 1 to 80
- Alignment No. 15463
- gi No. 2842627
- % Identity 77.8
- Alignment Length 81
- Location of Alignment in SEQ ID NO 2603: from 1 to 81
- Alignment No. 15464
- gi No. 3128195
- % Identity 90.1
- Alignment Length 81
- Location of Alignment in SEQ ID NO 2603: from 1 to 81
- Alignment No. 15465
- gi No. 4902849
- % Identity 96.3
- Alignment Length 81
- Location of Alignment in SEQ ID NO 2603: from 1 to 81
- Alignment No. 15466
- gi No. 4902851
- % Identity 91.4
- Alignment Length 81
- Location of Alignment in SEQ ID NO 2603: from 1 to 81
- (B) Polypeptide Sequence
 - Pat. Appln. SEQ ID NO 2604
 - Ceres seq id 1503948
 - Location of start within SEQ ID NO 2602: at 80 nt.
- (C) Nomination and Annotation of Domains within Predicted Polypeptide(s)
 - Alignment No. 15467
 - Phosphoribosyl pyrophosphate synthetase
 - Location within SEQ ID NO 2604: from 1 to 54 aa.
 - (D) Related Amino Acid Sequences
 - Alignment No. 15468
 - gi No. 2833379
 - % Identity 87.7
 - Alignment Length 81
 - Location of Alignment in SEQ ID NO 2604: from 1 to 55
 - Alignment No. 15469
 - gi No. 2833380
 - % Identity 87.7
 - Alignment Length 81
 - Location of Alignment in SEQ ID NO 2604: from 1 to 55

- Alignment No. 15470
- gi No. 2833468
- % Identity 76.3
- Alignment Length 80
- Location of Alignment in SEQ ID NO 2604: from 1 to 54
- Alignment No. 15471
- qi No. 2842627
- % Identity 77.8
- Alignment Length 81
- Location of Alignment in SEQ ID NO 2604: from 1 to 55
- Alignment No. 15472
- gi No. 3128195
- % Identity 90.1
- Alignment Length 81
- Location of Alignment in SEQ ID NO 2604: from 1 to 55
- Alignment No. 15473
- gi No. 4902849
- % Identity 96.3
- Alignment Length 81
- Location of Alignment in SEQ ID NO 2604: from 1 to 55
- Alignment No. 15474
- qi No. 4902851
- % Identity 91.4
- Alignment Length 81
- Location of Alignment in SEQ ID NO 2604: from 1 to 55
- (B) Polypeptide Sequence
 - Pat. Appln. SEQ ID NO 2605
 - Ceres seg id 1503949
 - Location of start within SEQ ID NO 2602: at 280 nt.
- - Alignment No. 15475
 - Phosphoribosyl pyrophosphate synthetase
 - Location within SEQ ID NO 2605: from 1 to 70 aa.
 - (D) Related Amino Acid Sequences
 - Alignment No. 15476
 - gi No. 4902849
 - % Identity 71.6
 - Alignment Length 116
 - Location of Alignment in SEQ ID NO 2605: from 1 to 70

- (A) Polynucleotide Sequence
 - Pat. Appln. SEQ ID NO 2606
 - Ceres seq_id 1503969
 - (B) Polypeptide Sequence
 - Pat. Appln. SEQ ID NO 2607
 - Ceres seq id 1503970
 - Location of start within SEQ ID NO 2606: at 1 nt.
- - (D) Related Amino Acid Sequences

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- Alignment No. 15477
- gi No. 4587514
- % Identity 94.9
- Alignment Length 59
- Location of Alignment in SEQ ID NO 2607: from 1 to 59
- Alignment No. 15478
- gi No. 5531833
- % Identity 71.2
- Alignment Length 59
- Location of Alignment in SEQ ID NO 2607: from 1 to 59
- Alignment No. 15479
- gi No. 5531851
- % Identity 71.2
- Alignment Length 59
- Location of Alignment in SEQ ID NO 2607: from 1 to 59
- (B) Polypeptide Sequence
 - Pat. Appln. SEQ ID NO 2608
 - Ceres seq_id 1503971
 - Location of start within SEQ ID NO 2606: at 34 nt.
- - (D) Related Amino Acid Sequences
 - Alignment No. 15480
 - gi No. 4587514
 - % Identity 94.9
 - Alignment Length 59
 - Location of Alignment in SEQ ID NO 2608: from 1 to 48
 - Alignment No. 15481
 - gi No. 5531833
 - % Identity 71.2
 - Alignment Length 59
 - Location of Alignment in SEQ ID NO 2608: from 1 to 48
 - Alignment No. 15482
 - gi No. 5531851
 - % Identity 71.2
 - Alignment Length 59
 - Location of Alignment in SEQ ID NO 2608: from 1 to 48
 - (B) Polypeptide Sequence
 - Pat. Appln. SEQ ID NO 2609
 - Ceres seq_id 1503972
 - Location of start within SEQ ID NO 2606: at 184 nt.
- - (D) Related Amino Acid Sequences

- (A) Polynucleotide Sequence
 - Pat. Appln. SEQ ID NO 2610
 - Ceres seq_id 1503989
 - (B) Polypeptide Sequence
 - Pat. Appln. SEQ ID NO 2611
 - Ceres seq_id 1503990
 - Location of start within SEQ ID NO 2610: at 67 nt.

- - Alignment No. 15483
 - EF hand
 - Location within SEQ ID NO 2611: from 48 to 76 aa.
 - (D) Related Amino Acid Sequences
 - Alignment No. 15484
 - gi No. 100665
 - % Identity 99.3
 - Alignment Length 146
 - Location of Alignment in SEQ ID NO 2611: from 1 to 145
 - Alignment No. 15485
 - gi No. 1076792
 - % Identity 97.9
 - Alignment Length 146
 - Location of Alignment in SEQ ID NO 2611: from 1 to 145
 - Alignment No. 15486
 - gi No. 1076793
 - % Identity 98.6
 - Alignment Length 146
 - Location of Alignment in SEQ ID NO 2611: from 1 to 145
 - Alignment No. 15487
 - gi No. 1084453
 - % Identity 98.6
 - Alignment Length 146
 - Location of Alignment in SEQ ID NO 2611: from 1 to 145
 - Alignment No. 15488
 - gi No. 1085679
 - % Identity 91.8
 - Alignment Length 146
 - Location of Alignment in SEQ ID NO 2611: from 1 to 145
 - Alignment No. 15489
 - gi No. 115480
 - % Identity 97.7
 - Alignment Length 133
 - Location of Alignment in SEQ ID NO 2611: from 14 to 145
 - Alignment No. 15490
 - gi No. 115484
 - % Identity 99.3
 - Alignment Length 146
 - Location of Alignment in SEQ ID NO 2611: from 1 to 145
 - Alignment No. 15491
 - gi No. 115486
 - % Identity 98.6
 - Alignment Length 146
 - Location of Alignment in SEQ ID NO 2611: from 1 to 145
 - Alignment No. 15492
 - gi No. 115489
 - % Identity 91.1
 - Alignment Length 146
 - Location of Alignment in SEQ ID NO 2611: from 1 to 145

- Alignment No. 15493
- gi No. 115492
- % Identity 99.3
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2611: from 1 to 145
- Alignment No. 15494
- gi No. 115500
- % Identity 91.9
- Alignment Length 135
- Location of Alignment in SEQ ID NO 2611: from 12 to 145
- Alignment No. 15495
- gi No. 115503
- % Identity 89.7
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2611: from 1 to 145
- Alignment No. 15496
- gi No. 115504
- % Identity 82.2
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2611: from 1 to 145
- Alignment No. 15497
- gi No. 115506
- % Identity 87.5
- . Alignment Length 144
 - Location of Alignment in SEQ ID NO 2611: from 3 to 145
 - Alignment No. 15498
 - gi No. 115508
 - % Identity 91.8
 - Alignment Length 146
 - Location of Alignment in SEQ ID NO 2611: from 1 to 145
 - Alignment No. 15499
 - gi No. 115509
 - % Identity 90.4
 - Alignment Length 146
 - Location of Alignment in SEQ ID NO 2611: from 1 to 145
 - Alignment No. 15500
 - gi No. 115510
 - % Identity 90.3
 - Alignment Length 145
 - Location of Alignment in SEQ ID NO 2611: from 2 to 145
 - Alignment No. 15501
 - gi No. 115511
 - % Identity 100
 - Alignment Length 146
 - Location of Alignment in SEQ ID NO 2611: from 1 to 145
 - Alignment No. 15502
 - gi No. 115513
 - % Identity 93.2
 - Alignment Length 146
 - Location of Alignment in SEQ ID NO 2611: from 1 to 145

- Alignment No. 15503
- gi No. 115514
- % Identity 80
- Alignment Length 30
- Location of Alignment in SEQ ID NO 2611: from 75 to 104
- Alignment No. 15504
- gi No. 115515
- % Identity 98.6
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2611: from 1 to 145
- Alignment No. 15505
- gi No. 115516
- % Identity 91
- Alignment Length 145
- Location of Alignment in SEQ ID NO 2611: from 2 to 145
- Alignment No. 15506
- gi No. 115518
- % Identity 90.3
- Alignment Length 145
- Location of Alignment in SEQ ID NO 2611: from 2 to 145
- Alignment No. 15507
- gi No. 115519
- % Identity 91.8
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2611: from 1 to 145
- Alignment No. 15508
- gi No. 115520
- % Identity 87
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2611: from 1 to 145
- Alignment No. 15509
- gi No. 115521
- % Identity 89.7
- Alignment Length 145
- Location of Alignment in SEQ ID NO 2611: from 2 to 145
- Alignment No. 15510
- gi No. 115522
- % Identity 91
- Alignment Length 145
- Location of Alignment in SEQ ID NO 2611: from 2 to 145
- Alignment No. 15511
- gi No. 115523
- % Identity 75.4
- Alignment Length 142
- Location of Alignment in SEQ ID NO 2611: from 5 to 145
- Alignment No. 15512
- gi No. 115524
- % Identity 92.5
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2611: from 1 to 145
- Alignment No. 15513

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- gi No. 115525
- % Identity 97.9
- Alignment Length 145
- Location of Alignment in SEQ ID NO 2611: from 2 to 145
- Alignment No. 15514
- qi No. 115526
- % Identity 91
- Alignment Length 145
- Location of Alignment in SEQ ID NO 2611: from 2 to 145
- Alignment No. 15515
- gi No. 115527
- % Identity 87
- Alignment Length 77
- Location of Alignment in SEQ ID NO 2611: from 70 to 145
- Alignment No. 15516
- gi No. 115528
- % Identity 90.4
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2611: from 1 to 145
- Alignment No. 15517
- gi No. 115530
- % Identity 90.4
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2611: from 1 to 145
- Alignment No. 15518
- gi No. 115531
- % Identity 91.1
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2611: from 1 to 145
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- Alignment No. 15519 - gi No. 115532
- % Identity 97.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2611: from 2 to 145
- Alignment No. 15520
- gi No. 115534
- % Identity 93.1
- Alignment Length 131
- Location of Alignment in SEQ ID NO 2611: from 12 to 142
- Alignment No. 15521
- gi No. 115541
- % Identity 83.6
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2611: from 1 to 145
- Alignment No. 15522
- gi No. 1168748
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2611: from 1 to 145
- Alignment No. 15523
- gi No. 1168749

- % Identity 98.6 - Alignment Length 146 - Location of Alignment in SEQ ID NO 2611: from 1 to 145 - Alignment No. 15524 - qi No. 1235664 - % Identity 85.6 - Alignment Length 146 - Location of Alignment in SEQ ID NO 2611: from 1 to 145 - Alignment No. 15525 - gi No. 1292710 - % Identity 97.3 - Alignment Length 147 - Location of Alignment in SEQ ID NO 2611: from 1 to 145 - Alignment No. 15526 - gi No. 1292853 - % Identity 88.4 - Alignment Length 146 - Location of Alignment in SEQ ID NO 2611: from 1 to 145 - Alignment No. 15527 - gi No. 1311052 - % Identity 88.6 - Alignment Length 70 - Location of Alignment in SEQ ID NO 2611: from 77 to 145 - Alignment No. 15528 - gi No. 1345451 - % Identity 94.8 - Alignment Length 58 - Location of Alignment in SEQ ID NO 2611: from 2 to 59 - Alignment No. 15529 - gi No. 1345660 - % Identity 98.6 - Alignment Length 146 - Location of Alignment in SEQ ID NO 2611: from 1 to 145 - Alignment No. 15530 - gi No. 1345661 - % Identity 87.7 - Alignment Length 146 - Location of Alignment in SEQ ID NO 2611: from 1 to 145 - Alignment No. 15531 - gi No. 1362058 - % Identity 96.6 - Alignment Length 146 - Location of Alignment in SEQ ID NO 2611: from 1 to 145 - Alignment No. 15532 - gi No. 1402947 - % Identity 97.9 - Alignment Length 146

- Location of Alignment in SEQ ID NO 2611: from 1 to 145

- Alignment No. 15533
- gi No. 1421816
- % Identity 85.5

- Alignment Length 145
- Location of Alignment in SEQ ID NO 2611: from 2 to 145
- Alignment No. 15534
- gi No. 1565285
- % Identity 93.2
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2611: from 1 to 145
- Alignment No. 15535
- gi No. 162030
- % Identity 89.7
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2611: from 1 to 145
- Alignment No. 15536
- gi No. 16225
- % Identity 99.3
- Alignment Length 135
- Location of Alignment in SEQ ID NO 2611: from 12 to 145
- Alignment No. 15537
- gi No. 166655
- % Identity 98.6
- Alignment Length 140
- Location of Alignment in SEQ ID NO 2611: from 7 to 145
- Alignment No. 15538
- gi No. 167676
- % Identity 87.4
- Alignment Length 135
- Location of Alignment in SEQ ID NO 2611: from 12 to 145 $\,$
- Alignment No. 15539
- gi No. 168777
- % Identity 82.2
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2611: from 1 to 145
- Alignment No. 15540
- gi No. 169406
- % Identity 88
- Alignment Length 75
- Location of Alignment in SEQ ID NO 2611: from 41 to 115
- Alignment No. 15541
- gi No. 170076
- % Identity 79.5
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2611: from 1 to 145
- Alignment No. 15542
- gi No. 1705567
- % Identity 85.4
- Alignment Length 144
- Location of Alignment in SEQ ID NO 2611: from 3 to 145
- Alignment No. 15543
- gi No. 1754997
- % Identity 98.3
- Alignment Length 121

- Location of Alignment in SEQ ID NO 2611: from 26 to 145
- Alignment No. 15544
- gi No. 1754999
- % Identity 98.6
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2611: from 1 to 145
- Alignment No. 15545
- gi No. 1785953
- % Identity 84.1
- Alignment Length 63
- Location of Alignment in SEQ ID NO 2611: from 57 to 119
- Alignment No. 15546
- gi No. 1785955
- % Identity 72.5
- Alignment Length 131
- Location of Alignment in SEQ ID NO 2611: from 16 to 145
- Alignment No. 15547
- gi No. 1785958
- % Identity 87.3
- Alignment Length 63
- Location of Alignment in SEQ ID NO 2611: from 57 to 119
- Alignment No. 15548
- gi No. 20186
- % Identity 99.3
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2611: from 1 to 145
- Alignment No. 15549
- gi No. 208092
- % Identity 96.6
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2611: from 1 to 145
- Alignment No. 15550
- gi No. 2119350
- % Identity 92.2
- Alignment Length 51
- Location of Alignment in SEQ ID NO 2611: from 77 to 127
- Alignment No. 15551
- gi No. 2119353
- % Identity 91.8
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2611: from 1 to 145
- Alignment No. 15552
- gi No. 2119360
- % Identity 99.2
- Alignment Length 121
- Location of Alignment in SEQ ID NO 2611: from 26 to 145
- Alignment No. 15553
- gi No. 2119361
- % Identity 94.2
- Alignment Length 121
- Location of Alignment in SEQ ID NO 2611: from 26 to 145

- Alignment No. 15554
- gi No. 2119362
- % Identity 90.4
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2611: from 1 to 145
- Alignment No. 15555
- gi No. 2119364
- % Identity 90
- Alignment Length 20
- Location of Alignment in SEQ ID NO 2611: from 94 to 113
- Alignment No. 15556
- gi No. 2129557
- % Identity 96.8
- Alignment Length 31
- Location of Alignment in SEQ ID NO 2611: from 1 to 31
- Alignment No. 15557
- gi No. 2129558
- % Identity 93.5
- Alignment Length 31
- Location of Alignment in SEQ ID NO 2611: from 1 to 31
- Alignment No. 15558
- gi No. 2129978
- % Identity 97.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2611: from 1 to 145
- Alignment No. 15559
- gi No. 2147165
- % Identity 98.6
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2611: from 1 to 145
- Alignment No. 15560
- gi No. 2181205
- % Identity 92.5
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2611: from 1 to 145
- Alignment No. 15561
- gi No. 222925
- % Identity 92.6
- Alignment Length 136
- Location of Alignment in SEQ ID NO 2611: from 8 to 143
- Alignment No. 15562
- gi No. 223036
- % Identity 88.3
- Alignment Length 145
- Location of Alignment in SEQ ID NO 2611: from 2 to 145
- Alignment No. 15563
- gi No. 223218
- % Identity 89
- Alignment Length 145
- Location of Alignment in SEQ ID NO 2611: from 2 to 145

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- Alignment No. 15564
- gi No. 223872
- % Identity 86.9
- Alignment Length 145
- Location of Alignment in SEQ ID NO 2611: from 2 to 145
- Alignment No. 15565
- gi No. 2244820
- % Identity 75.4
- Alignment Length 142
- Location of Alignment in SEQ ID NO 2611: from 5 to 145
- Alignment No. 15566
- gi No. 225024
- % Identity 87.5
- Alignment Length 144
- Location of Alignment in SEQ ID NO 2611: from 3 to 145
- Alignment No. 15567
- gi No. 2267084
- % Identity 94.1
- Alignment Length 135
- Location of Alignment in SEQ ID NO 2611: from 12 to 145
- Alignment No. 15568
- gi No. 228408
- % Identity 97.7
- Alignment Length 133
- Location of Alignment in SEQ ID NO 2611: from 14 to 145
- Alignment No. 15569
- gi No. 2291247
- % Identity 91.8
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2611: from 1 to 145
- Alignment No. 15570
 - gi No. 230381
 - % Identity 88.2
 - Alignment Length 68
 - Location of Alignment in SEQ ID NO 2611: from 79 to 145
 - Alignment No. 15571
 - gi No. 230382
 - % Identity 86.4
 - Alignment Length 66
 - Location of Alignment in SEQ ID NO 2611: from 81 to 145
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- Alignment No. 15572
- gi No. 2388889
- % Identity 99.2
- Alignment Length 118
- Location of Alignment in SEQ ID NO 2611: from 9 to 126
- Alignment No. 15573
- gi No. 2388891
- % Identity 95.2
- Alignment Length 104
- Location of Alignment in SEQ ID NO 2611: from 1 to 104
- Alignment No. 15574

- gi No. 2392137
- % Identity 90.3
- Alignment Length 145
- Location of Alignment in SEQ ID NO 2611: from 2 to 145
- Alignment No. 15575
- qi No. 2464957
- % Identity 89.5
- Alignment Length 86
- Location of Alignment in SEQ ID NO 2611: from 61 to 145
- Alignment No. 15576
- gi No. 249170
- % Identity 92.3
- Alignment Length 39
- Location of Alignment in SEQ ID NO 2611: from 32 to 70
- Alignment No. 15577
- gi No. 249171
- % Identity 75.4
- Alignment Length 61
- Location of Alignment in SEQ ID NO 2611: from 77 to 133
- Alignment No. 15578
- gi No. 254773
- % Identity 100
- Alignment Length 20
- Location of Alignment in SEQ ID NO 2611: from 108 to 127
- Alignment No. 15579
- gi No. 2554673
- % Identity 93.3
- Alignment Length 75
- Location of Alignment in SEQ ID NO 2611: from 2 to 76
- Alignment No. 15580
- gi No. 2623680
- % Identity 98.6
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2611: from 1 to 145
- Alignment No. 15581
- gi No. 2654179
- % Identity 93
- Alignment Length 86
- Location of Alignment in SEQ ID NO 2611: from 38 to 123
- Alignment No. 15582
- gi No. 266018
- % Identity 91.2
- Alignment Length 34
- Location of Alignment in SEQ ID NO 2611: from 96 to 129
- Alignment No. 15583
- qi No. 2677834
- % Identity 93.6
- Alignment Length 110
- Location of Alignment in SEQ ID NO 2611: from 20 to 129
- Alignment No. 15584
- qi No. 2809481

- % Identity 98.6

- Alignment Length 146

- Location of Alignment in SEQ ID NO 2611: from 1 to 145
- Alignment No. 15585
- qi No. 2832598
- % Identity 91.8
- Alignment Length 134
- Location of Alignment in SEQ ID NO 2611: from 8 to 141
- Alignment No. 15586
- gi No. 289525
- % Identity 98.6
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2611: from 1 to 145
- Alignment No. 15587
- gi No. 2959326
- % Identity 71.7
- Alignment Length 130
- Location of Alignment in SEQ ID NO 2611: from 8 to 129
- Alignment No. 15588
- gi No. 3021331
- % Identity 83.8
- Alignment Length 68
- Location of Alignment in SEQ ID NO 2611: from 74 to 141
- Alignment No. 15589
- gi No. 310563
- % Identity 78.8
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2611: from 1 to 145
- Alignment No. 15590
- gi No. 3121848
- % Identity 98.6
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2611: from 1 to 145
- Alignment No. 15591
- gi No. 3121849
- % Identity 98.6
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2611: from 1 to 145
- Alignment No. 15592
- gi No. 3136336
- % Identity 98.6
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2611: from 1 to 145
- Alignment No. 15593
- gi No. 3243222
- % Identity 88.6
- Alignment Length 35
- Location of Alignment in SEQ ID NO 2611: from 77 to 111
- Alignment No. 15594
- gi No. 3336912
- % Identity 93.8

- Alignment Length 146
- Location of Alignment in SEQ ID NO 2611: from 1 to 145
- Alignment No. 15595
- gi No. 3378652
- % Identity 100
- Alignment Length 119
- Location of Alignment in SEQ ID NO 2611: from 28 to 145
- Alignment No. 15596
- gi No. 3415119
- % Identity 89.7
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2611: from 1 to 145
- Alignment No. 15597
- gi No. 348265
- % Identity 100
- Alignment Length 29
- Location of Alignment in SEQ ID NO 2611: from 32 to 60
- Alignment No. 15598
- gi No. 348267
- % Identity 94.7
- Alignment Length 19
- Location of Alignment in SEQ ID NO 2611: from 108 to 126
- Alignment No. 15599
- gi No. 348268
- % Identity 78.9
- Alignment Length 19
- Location of Alignment in SEQ ID NO 2611: from 128 to 145
- Alignment No. 15600
- gi No. 3561059
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2611: from 1 to 145
- Alignment No. 15601
- gi No. 3561061
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2611: from 1 to 145
- Alignment No. 15602
- gi No. 3786339
- % Identity 91.1
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2611: from 1 to 145
- Alignment No. 15603
- gi No. 3800845
- % Identity 82.2
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2611: from 1 to 145
- Alignment No. 15604
- gi No. 3800847
- % Identity 74.7 - Alignment Length 146

- Location of Alignment in SEQ ID NO 2611: from 1 to 145
- Alignment No. 15605
- gi No. 3800849
- % Identity 87.7
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2611: from 1 to 145
- Alignment No. 15606
- gi No. 3800851
- % Identity 72.6
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2611: from 1 to 145
- Alignment No. 15607
- gi No. 3913191
- % Identity 97.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2611: from 1 to 145
- Alignment No. 15608
- gi No. 4028590
- % Identity 82.2
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2611: from 1 to 145
- Alignment No. 15609
- gi No. 4033343
- % Identity 82.1
- Alignment Length 145
- Location of Alignment in SEQ ID NO 2611: from 2 to 145
- Alignment No. 15610
- gi No. 4033509
- % Identity 90.4
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2611: from 1 to 145
- Alignment No. 15611
- gi No. 4098293
- % Identity 95.3
- Alignment Length 107
- Location of Alignment in SEQ ID NO 2611: from 20 to 126
- Alignment No. 15612
- gi No. 4098295
- % Identity 86
- Alignment Length 107
- Location of Alignment in SEQ ID NO 2611: from 20 to 126
- Alignment No. 15613
- gi No. 4103778
- % Identity 94.1
- Alignment Length 17
- Location of Alignment in SEQ ID NO 2611: from 130 to 145
- Alignment No. 15614
- gi No. 4103959
- % Identity 97.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2611: from 1 to 145

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- Alignment No. 15615 - gi No. 4103963 - % Identity 100 - Alignment Length 65 - Location of Alignment in SEQ ID NO 2611: from 82 to 145 - Alignment No. 15616 - gi No. 4103965 - % Identity 100 - Alignment Length 64 - Location of Alignment in SEQ ID NO 2611: from 83 to 145 - Alignment No. 15617 - gi No. 4150908 - % Identity 90.4 - Alignment Length 146 - Location of Alignment in SEQ ID NO 2611: from 1 to 145 - Alignment No. 15618 - gi No. 4200039 - % Identity 88.4 - Alignment Length 146 - Location of Alignment in SEQ ID NO 2611: from 1 to 145 - Alignment No. 15619 - gi No. 4335787 - % Identity 90.4 - Alignment Length 146 - Location of Alignment in SEQ ID NO 2611: from 1 to 145 - Alignment No. 15620 - gi No. 4336136 - % Identity 87.2 - Alignment Length 47 - Location of Alignment in SEQ ID NO 2611: from 21 to 67 - Alignment No. 15621 - gi No. 4379369 - % Identity 93.2 - Alignment Length 146 - Location of Alignment in SEQ ID NO 2611: from 1 to 145 - Alignment No. 15622 - gi No. 443167 - % Identity 87.6 - Alignment Length 145 - Location of Alignment in SEQ ID NO 2611: from 2 to 145 - Alignment No. 15623 - gi No. 4468115 - % Identity 91.1 - Alignment Length 146 - Location of Alignment in SEQ ID NO 2611: from 1 to 145
- Alignment No. 15624
- gi No. 4502549
- % Identity 91.1
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2611: from 1 to 145

- Alignment No. 15625 - gi No. 4581211 - % Identity 87 - Alignment Length 77 - Location of Alignment in SEQ ID NO 2611: from 70 to 145 - Alignment No. 15626 - gi No. 4581213 - % Identity 78.1 - Alignment Length 146 - Location of Alignment in SEQ ID NO 2611: from 1 to 145 - Alignment No. 15627 - gi No. 4585219 - % Identity 82.2 - Alignment Length 146 - Location of Alignment in SEQ ID NO 2611: from 1 to 145 - Alignment No. 15628 - qi No. 461684 - % Identity 85.1 - Alignment Length 148 - Location of Alignment in SEQ ID NO 2611: from 1 to 145 - Alignment No. 15629 - gi No. 476851 - % Identity 85.7 - Alignment Length 77 - Location of Alignment in SEQ ID NO 2611: from 70 to 145 - Alignment No. 15630 - qi No. 484660 - % Identity 82.4 - Alignment Length 142 - Location of Alignment in SEQ ID NO 2611: from 3 to 144 - Alignment No. 15631 - gi No. 4885109 - % Identity 89.3 - Alignment Length 149 - Location of Alignment in SEQ ID NO 2611: from 1 to 145 - Alignment No. 15632 - gi No. 4885111 - % Identity 82.9 - Alignment Length 146 - Location of Alignment in SEQ ID NO 2611: from 1 to 145 - Alignment No. 15633 - gi No. 4930156 - % Identity 95.9 - Alignment Length 145 - Location of Alignment in SEQ ID NO 2611: from 2 to 145 - Alignment No. 15634 - gi No. 4959142 - % Identity 94.5

- Location of Alignment in SEQ ID NO 2611: from 1 to 145

- Alignment No. 15635

- Alignment Length 146

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- gi No. 4959143
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2611: from 1 to 145
- Alignment No. 15636
- gi No. 4959144
- % Identity 95.2
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2611: from 1 to 145
- Alignment No. 15637
- gi No. 4959145
- % Identity 97.3
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2611: from 1 to 145
- Alignment No. 15638
- qi No. 4959146
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2611: from 1 to 145
- Alignment No. 15639
- gi No. 4959147
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2611: from 1 to 145
- Alignment No. 15640
- gi No. 4959148
- % Identity 94
- Alignment Length 149
- Location of Alignment in SEQ ID NO 2611: from 1 to 145
- Alignment No. 15641
- gi No. 4959149
- % Identity 95.2
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2611: from 1 to 145
- Alignment No. 15642
- gi No. 4959150
- % Identity 95.2
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2611: from 1 to 145
- Alignment No. 15643
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- Alignment No. 15644
- gi No. 4959152

- gi No. 4959151
- % Identity 95.2
- Alignment Length 146

- % Identity 93.2
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2611: from 1 to 145

- Location of Alignment in SEQ ID NO 2611: from 1 to 145

- Alignment No. 15645
- gi No. 4959153

- % Identity 93.2 - Alignment Length 146
- Location of Alignment in SEQ ID NO 2611: from 1 to 145
- Alignment No. 15646
- gi No. 4959154
- % Identity 92.5
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2611: from 1 to 145
- Alignment No. 15647
- gi No. 4959155
- % Identity 92.5
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2611: from 1 to 145
- Alignment No. 15648
- gi No. 4959156
- % Identity 93.2
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2611: from 1 to 145
- Alignment No. 15649
- gi No. 4959157
- % Identity 91.8
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2611: from 1 to 145
- Alignment No. 15650
- gi No. 4959159
- % Identity 89
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2611: from 1 to 145
- Alignment No. 15651
- gi No. 4959160
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2611: from 1 to 145
- Alignment No. 15652
- gi No. 4959161
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2611: from 1 to 145
- Alignment No. 15653
- gi No. 4959162
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2611: from 1 to 145
- Alignment No. 15654
- qi No. 4959163
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2611: from 1 to 145
- Alignment No. 15655
- gi No. 4959164
- % Identity 95.9

- Alignment Length 146
- Location of Alignment in SEQ ID NO 2611: from 1 to 145
- Alignment No. 15656
- gi No. 4959165
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2611: from 1 to 145
- Alignment No. 15657
- qi No. 4959166
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2611: from 1 to 145
- Alignment No. 15658
- gi No. 4959167
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2611: from 1 to 145
- Alignment No. 15659
- gi No. 4959168
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2611: from 1 to 145
- Alignment No. 15660
- gi No. 4959169
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2611: from 1 to 145
- Alignment No. 15661
- gi No. 4959170
- % Identity 95.2
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2611: from 1 to 145
- Alignment No. 15662
- gi No. 4959171
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2611: from 1 to 145
- Alignment No. 15663
- gi No. 4959172
- % Identity 96.6
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2611: from 1 to 145
- Alignment No. 15664
- gi No. 4959588
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2611: from 1 to 145
- Alignment No. 15665
- gi No. 4959590
- % Identity 95.9
- Alignment Length 146

- Location of Alignment in SEQ ID NO 2611: from 1 to 145
- Alignment No. 15666
- gi No. 4959593
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2611: from 1 to 145
- Alignment No. 15667
- gi No. 4959594
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2611: from 1 to 145
- Alignment No. 15668
- gi No. 4959598
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2611: from 1 to 145
- Alignment No. 15669
- gi No. 4959599
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2611: from 1 to 145
- Alignment No. 15670
- gi No. 4959600
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2611: from 1 to 145
- Alignment No. 15671
- gi No. 4959602
- % Identity 94.5
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2611: from 1 to 145
- Alignment No. 15672
- gi No. 4959604
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2611: from 1 to 145
- Alignment No. 15673
- qi No. 4959612
- % Identity 93.8
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2611: from 1 to 145
- Alignment No. 15674
- gi No. 4959613
- % Identity 91.8
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2611: from 1 to 145
- Alignment No. 15675
- gi No. 4959614
- % Identity 95.2
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2611: from 1 to 145

- Alignment No. 15676 - gi No. 4959615 - % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2611: from 1 to 145
- Alignment No. 15677
- gi No. 4959616
- % Identity 94.5
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2611: from 1 to 145
- Alignment No. 15678
- gi No. 4959617
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2611: from 1 to 145
- Alignment No. 15679
- gi No. 4959618
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2611: from 1 to 145
- Alignment No. 15680
- gi No. 4959621
- % Identity 94.5
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2611: from 1 to 145
- Alignment No. 15681
- gi No. 4959622
- % Identity 92.5
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2611: from 1 to 145
- Alignment No. 15682
- gi No. 4959625
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2611: from 1 to 145
- Alignment No. 15683
- gi No. 4959626
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2611: from 1 to 145
- Alignment No. 15684
- gi No. 4959629
- % Identity 94.6
- Alignment Length 149
- Location of Alignment in SEQ ID NO 2611: from 1 to 145
- Alignment No. 15685
- gi No. 4959630
- % Identity 95.2
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2611: from 1 to 145

- Alignment No. 15686
- gi No. 4959635
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2611: from 1 to 145
- Alignment No. 15687
- qi No. 4959636
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2611: from 1 to 145
- Alignment No. 15688
- gi No. 4959637
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2611: from 1 to 145
- Alignment No. 15689
- gi No. 4959638
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2611: from 1 to 145
- Alignment No. 15690
- gi No. 4959640
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2611: from 1 to 145
- Alignment No. 15691
- gi No. 4959645
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2611: from 1 to 145
- Alignment No. 15692
- gi No. 4959646
- % Identity 96.6
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2611: from 1 to 145
- Alignment No. 15693
- gi No. 4959647
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2611: from 1 to 145
- Alignment No. 15694
- gi No. 4959648
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2611: from 1 to 145
- Alignment No. 15695
- gi No. 4995673
- % Identity 100
- Alignment Length 22
- Location of Alignment in SEQ ID NO 2611: from 49 to 70
- Alignment No. 15696

- qi No. 4995696
- % Identity 95.5
- Alignment Length 22
- Location of Alignment in SEQ ID NO 2611: from 49 to 70
- Alignment No. 15697
- gi No. 4995737
- % Identity 82.6
- Alignment Length 23
- Location of Alignment in SEQ ID NO 2611: from 49 to 71
- Alignment No. 15698
- gi No. 4995739
- % Identity 91.3
- Alignment Length 23
- Location of Alignment in SEQ ID NO 2611: from 49 to 71
- Alignment No. 15699
- qi No. 508526
- % Identity 90.8
- Alignment Length 131
- Location of Alignment in SEQ ID NO 2611: from 1 to 131
- Alignment No. 15700
- gi No. 535428
- % Identity 76
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2611: from 1 to 145
- Alignment No. 15701
- gi No. 552252
- % Identity 84.6
- Alignment Length 26
- Location of Alignment in SEQ ID NO 2611: from 75 to 100
- Alignment No. 15702
- gi No. 5640002
- % Identity 91.3
- Alignment Length 80
- Location of Alignment in SEQ ID NO 2611: from 61 to 140
- Alignment No. 15703
- gi No. 565166
- % Identity 86.2
- Alignment Length 145
- Location of Alignment in SEQ ID NO 2611: from 2 to 145
- Alignment No. 15704
- gi No. 576081
- % Identity 89.4
- Alignment Length 141
- Location of Alignment in SEQ ID NO 2611: from 6 to 145
- Alignment No. 15705
- gi No. 587454
- % Identity 90.5
- Alignment Length 137
- Location of Alignment in SEQ ID NO 2611: from 10 to 145
- Alignment No. 15706
- gi No. 625985

- % Identity 95.7 - Alignment Length 46
- Location of Alignment in SEQ ID NO 2611: from 1 to 46
- Alignment No. 15707
- gi No. 640285
- % Identity 91
- Alignment Length 145
- Location of Alignment in SEQ ID NO 2611: from 2 to 145
- Alignment No. 15708
- gi No. 640294
- % Identity 90.8
- Alignment Length 142
- Location of Alignment in SEQ ID NO 2611: from 5 to 145
- Alignment No. 15709
- gi No. 71660
- % Identity 90.3
- Alignment Length 145
- Location of Alignment in SEQ ID NO 2611: from 2 to 145
- Alignment No. 15710
- gi No. 71662
- % Identity 91
- Alignment Length 145
- Location of Alignment in SEQ ID NO 2611: from 2 to 145
- Alignment No. 15711
- gi No. 71667
- % Identity 91.7
- Alignment Length 145
- Location of Alignment in SEQ ID NO 2611: from 2 to 145
- Alignment No. 15712
- gi No. 71673
- % Identity 90.3
- Alignment Length 145
- Location of Alignment in SEQ ID NO 2611: from 2 to 145
- Alignment No. 15713
- gi No. 71676
- % Identity 84.8
- Alignment Length 145
- Location of Alignment in SEQ ID NO 2611: from 2 to 145
- Alignment No. 15714
- gi No. 729010
- % Identity 98.6
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2611: from 1 to 145
- Alignment No. 15715
- gi No. 729011
- % Identity 82.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2611: from 1 to 145
- Alignment No. 15716
- gi No. 729012
- % Identity 87.3



- Location of Alignment in SEQ ID NO 2611: from 5 to 145
- Alignment No. 15717
- gi No. 809298
- % Identity 86.9
- Alignment Length 145
- Location of Alignment in SEQ ID NO 2611: from 2 to 145
- Alignment No. 15718
- gi No. 85332
- % Identity 92.2
- Alignment Length 141
- Location of Alignment in SEQ ID NO 2611: from 2 to 142
- Alignment No. 15719
- gi No. 9874
- % Identity 85.6
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2611: from 1 to 145
- Alignment No. 15720
- gi No. 99673
- % Identity 81.9
- Alignment Length 72
- Location of Alignment in SEQ ID NO 2611: from 3 to 74
- (B) Polypeptide Sequence
 - Pat. Appln. SEQ ID NO 2612
 - Ceres seq id 1503991
 - Location of start within SEQ ID NO 2610: at 175 nt.
- (C) Nomination and Annotation of Domains within Predicted Polypeptide(s)
 - Alignment No. 15721
 - EF hand
 - Location within SEQ ID NO 2612: from 12 to 40 aa.
 - (D) Related Amino Acid Sequences
 - Alignment No. 15722
 - gi No. 100665
 - % Identity 99.3
 - Alignment Length 146
 - Location of Alignment in SEQ ID NO 2612: from 1 to 109
 - Alignment No. 15723
 - gi No. 1076792
 - % Identity 97.9
 - Alignment Length 146
 - Location of Alignment in SEQ ID NO 2612: from 1 to 109
 - Alignment No. 15724
 - gi No. 1076793
 - % Identity 98.6
 - Alignment Length 146
 - Location of Alignment in SEQ ID NO 2612: from 1 to 109
 - Alignment No. 15725
 - gi No. 1084453
 - % Identity 98.6
 - Alignment Length 146

- Location of Alignment in SEQ ID NO 2612: from 1 to 109
- Alignment No. 15726
- gi No. 1085679
- % Identity 91.8
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2612: from 1 to 109
- Alignment No. 15727
- gi No. 115480
- % Identity 97.7
- Alignment Length 133
- Location of Alignment in SEQ ID NO 2612: from 1 to 109
- Alignment No. 15728
- gi No. 115484
- % Identity 99.3
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2612: from 1 to 109
- Alignment No. 15729
- gi No. 115486
- % Identity 98.6
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2612: from 1 to 109
- Alignment No. 15730
- gi No. 115489
- % Identity 91.1
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2612: from 1 to 109
- Alignment No. 15731
- gi No. 115492
- % Identity 99.3
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2612: from 1 to 109
- Alignment No. 15732
- gi No. 115500
- % Identity 91.9
- Alignment Length 135
- Location of Alignment in SEQ ID NO 2612: from 1 to 109
- Alignment No. 15733
- gi No. 115503
- % Identity 89.7
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2612: from 1 to 109
- Alignment No. 15734
- gi No. 115504
- % Identity 82.2
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2612: from 1 to 109
- Alignment No. 15735
- gi No. 115506
- % Identity 87.5
- Alignment Length 144
- Location of Alignment in SEQ ID NO 2612: from 1 to 109

- Alignment No. 15736
- gi No. 115508
- % Identity 91.8
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2612: from 1 to 109
- Alignment No. 15737
- gi No. 115509
- % Identity 90.4
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2612: from 1 to 109
- Alignment No. 15738
- gi No. 115510
- % Identity 90.3
- Alignment Length 145
- Location of Alignment in SEQ ID NO 2612: from 1 to 109
- Alignment No. 15739
- gi No. 115511
- % Identity 100
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2612: from 1 to 109
- Alignment No. 15740
- gi No. 115513
- % Identity 93.2
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2612: from 1 to 109
- Alignment No. 15741
- qi No. 115514
- % Identity 80
- Alignment Length 30
- Location of Alignment in SEQ ID NO 2612: from 39 to 68
- Alignment No. 15742
- gi No. 115515
- % Identity 98.6
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2612: from 1 to 109
- Alignment No. 15743
- gi No. 115516
- % Identity 91
- Alignment Length 145
- Location of Alignment in SEQ ID NO 2612: from 1 to 109
- Alignment No. 15744
- gi No. 115518
- % Identity 90.3
- Alignment Length 145
- Location of Alignment in SEQ ID NO 2612: from 1 to 109
- Alignment No. 15745
- gi No. 115519
- % Identity 91.8
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2612: from 1 to 109

- Alignment No. 15746
- gi No. 115520
- % Identity 87
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2612: from 1 to 109
- Alignment No. 15747
- gi No. 115521
- % Identity 89.7
- Alignment Length 145
- Location of Alignment in SEQ ID NO 2612: from 1 to 109
- Alignment No. 15748
- gi No. 115522
- % Identity 91
- Alignment Length 145
- Location of Alignment in SEQ ID NO 2612: from 1 to 109
- Alignment No. 15749
- gi No. 115523
- % Identity 75.4
- Alignment Length 142
- Location of Alignment in SEQ ID NO 2612: from 1 to 109
- Alignment No. 15750
- gi No. 115524
- % Identity 92.5
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2612: from 1 to 109
- Alignment No. 15751
- gi No. 115525
- % Identity 97.9
- Alignment Length 145
- Location of Alignment in SEQ ID NO 2612: from 1 to 109
- Alignment No. 15752
- gi No. 115526
- % Identity 91
- Alignment Length 145
- Location of Alignment in SEQ ID NO 2612: from 1 to 109
- Alignment No. 15753
- gi No. 115527
- % Identity 87
- Alignment Length 77
- Location of Alignment in SEQ ID NO 2612: from 34 to 109
- Alignment No. 15754
- gi No. 115528
- % Identity 90.4
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2612: from 1 to 109
- Alignment No. 15755
- gi No. 115530
- % Identity 90.4
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2612: from 1 to 109
- Alignment No. 15756

- gi No. 115531 - % Identity 91.1 - Alignment Length 146 - Location of Alignment in SEQ ID NO 2612: from 1 to 109 - Alignment No. 15757 - gi No. 115532 - % Identity 97.9 - Alignment Length 146 - Location of Alignment in SEQ ID NO 2612: from 1 to 109 - Alignment No. 15758 - gi No. 115534 - % Identity 93.1 - Alignment Length 131 - Location of Alignment in SEQ ID NO 2612: from 1 to 106 - Alignment No. 15759 - gi No. 115541 - % Identity 83.6 - Alignment Length 146 - Location of Alignment in SEQ ID NO 2612: from 1 to 109 - Alignment No. 15760 - gi No. 1168748 - % Identity 95.9 - Alignment Length 146 - Location of Alignment in SEQ ID NO 2612: from 1 to 109 - Alignment No. 15761 - gi No. 1168749 - % Identity 98.6 - Alignment Length 146 - Location of Alignment in SEQ ID NO 2612: from 1 to 109 - Alignment No. 15762 - gi No. 1235664 - % Identity 85.6 - Alignment Length 146 - Location of Alignment in SEQ ID NO 2612: from 1 to 109 - Alignment No. 15763 - gi No. 1292710 - % Identity 97.3 - Alignment Length 147 - Location of Alignment in SEQ ID NO 2612: from 1 to 109 - Alignment No. 15764 - gi No. 1292853 - % Identity 88.4 - Alignment Length 146 - Location of Alignment in SEQ ID NO 2612: from 1 to 109
- Alignment No. 15765
- gi No. 1311052
- % Identity 88.6
- Alignment Length 70
- Location of Alignment in SEQ ID NO 2612: from 41 to 109
- Alignment No. 15766
- gi No. 1345451

- % Identity 94.8
- Alignment Length 58
- Location of Alignment in SEQ ID NO 2612: from 1 to 23
- Alignment No. 15767
- gi No. 1345660
- % Identity 98.6
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2612: from 1 to 109
- Alignment No. 15768
- gi No. 1345661
- % Identity 87.7
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2612: from 1 to 109
- Alignment No. 15769
- gi No. 1362058
- % Identity 96.6
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2612: from 1 to 109
- Alignment No. 15770
- gi No. 1402947
- % Identity 97.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2612: from 1 to 109
- Alignment No. 15771
- gi No. 1421816
- % Identity 85.5
- Alignment Length 145
- Location of Alignment in SEQ ID NO 2612: from 1 to 109 $\,$
- Alignment No. 15772
- gi No. 1565285
- % Identity 93.2
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2612: from 1 to 109
- Alignment No. 15773
- gi No. 162030
- % Identity 89.7
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2612: from 1 to 109
- Alignment No. 15774
- gi No. 16225
- % Identity 99.3
- Alignment Length 135
- Location of Alignment in SEQ ID NO 2612: from 1 to 109
- Alignment No. 15775
- gi No. 166655
- % Identity 98.6
- Alignment Length 140
- Location of Alignment in SEQ ID NO 2612: from 1 to 109
- Alignment No. 15776
- gi No. 167676
- % Identity 87.4

- Alignment Length 135
- Location of Alignment in SEQ ID NO 2612: from 1 to 109
- Alignment No. 15777
- gi No. 168777
- % Identity 82.2
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2612: from 1 to 109
- Alignment No. 15778
- gi No. 169406
- % Identity 88
- Alignment Length 75
- Location of Alignment in SEQ ID NO 2612: from 5 to 79
- Alignment No. 15779
- gi No. 170076
- % Identity 79.5
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2612: from 1 to 109
- Alignment No. 15780
- qi No. 1705567
- % Identity 85.4
- Alignment Length 144
- Location of Alignment in SEQ ID NO 2612: from 1 to 109
- Alignment No. 15781
- gi No. 1754997
- % Identity 98.3
- Alignment Length 121
- Location of Alignment in SEQ ID NO 2612: from 1 to 109
- Alignment No. 15782
- gi No. 1754999
- % Identity 98.6
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2612: from 1 to 109
- Alignment No. 15783
- gi No. 1785953
- % Identity 84.1
- Alignment Length 63
- Location of Alignment in SEQ ID NO 2612: from 21 to 83
- Alignment No. 15784
- gi No. 1785955
- % Identity 72.5
- Alignment Length 131
- Location of Alignment in SEQ ID NO 2612: from 1 to 109
- Alignment No. 15785
- gi No. 1785958
- % Identity 87.3
- Alignment Length 63
- Location of Alignment in SEQ ID NO 2612: from 21 to 83
- Alignment No. 15786
- gi No. 20186
- % Identity 99.3
- Alignment Length 146

- Location of Alignment in SEQ ID NO 2612: from 1 to 109
- Alignment No. 15787
- qi No. 208092
- % Identity 96.6
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2612: from 1 to 109
- Alignment No. 15788
- gi No. 2119350
- % Identity 92.2
- Alignment Length 51
- Location of Alignment in SEQ ID NO 2612: from 41 to 91
- Alignment No. 15789
- gi No. 2119353
- % Identity 91.8
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2612: from 1 to 109
- Alignment No. 15790
- gi No. 2119360
- % Identity 99.2
- Alignment Length 121
- Location of Alignment in SEQ ID NO 2612: from 1 to 109
- Alignment No. 15791
- gi No. 2119361
- % Identity 94.2
- Alignment Length 121
- Location of Alignment in SEQ ID NO 2612: from 1 to 109
- Alignment No. 15792
- gi No. 2119362
- % Identity 90.4
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2612: from 1 to 109
- Alignment No. 15793
- gi No. 2119364
- % Identity 90
- Alignment Length 20
- Location of Alignment in SEQ ID NO 2612: from 58 to 77
- Alignment No. 15794
- gi No. 2129978
- % Identity 97.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2612: from 1 to 109
- Alignment No. 15795
- gi No. 2147165
- % Identity 98.6
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2612: from 1 to 109
- Alignment No. 15796
- gi No. 2181205
- % Identity 92.5
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2612: from 1 to 109

- Alignment No. 15797
- gi No. 222925
- % Identity 92.6
- Alignment Length 136
- Location of Alignment in SEQ ID NO 2612: from 1 to 107
- Alignment No. 15798
- gi No. 223036
- % Identity 88.3
- Alignment Length 145
- Location of Alignment in SEQ ID NO 2612: from 1 to 109
- Alignment No. 15799
- gi No. 223218
- % Identity 89
- Alignment Length 145
- Location of Alignment in SEQ ID NO 2612: from 1 to 109
- Alignment No. 15800
- gi No. 223872
- % Identity 86.9
- Alignment Length 145
- Location of Alignment in SEQ ID NO 2612: from 1 to 109
- Alignment No. 15801
- gi No. 2244820
- % Identity 75.4
- Alignment Length 142
- Location of Alignment in SEQ ID NO 2612: from 1 to 109
- Alignment No. 15802
- qi No. 225024
- % Identity 87.5
- Alignment Length 144
- Location of Alignment in SEQ ID NO 2612: from 1 to 109
- Alignment No. 15803
- gi No. 2267084
- % Identity 94.1
- Alignment Length 135
- Location of Alignment in SEQ ID NO 2612: from 1 to 109
- Alignment No. 15804
- gi No. 228408
- % Identity 97.7
- Alignment Length 133
- Location of Alignment in SEQ ID NO 2612: from 1 to 109
- Alignment No. 15805
- gi No. 2291247
- % Identity 91.8
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2612: from 1 to 109
- Alignment No. 15806
- gi No. 230381
- % Identity 88.2
- Alignment Length 68
- Location of Alignment in SEQ ID NO 2612: from 43 to 109

- Alignment No. 15807gi No. 230382% Identity 86.4Alignment Length 66
- Location of Alignment in SEQ ID NO 2612: from 45 to 109
- Alignment No. 15808
- gi No. 2388889
- % Identity 99.2
- Alignment Length 118
- Location of Alignment in SEQ ID NO 2612: from 1 to 90
- Alignment No. 15809
- gi No. 2388891
- % Identity 95.2
- Alignment Length 104
- Location of Alignment in SEQ ID NO 2612: from 1 to 68
- Alignment No. 15810
- gi No. 2392137
- % Identity 90.3
- Alignment Length 145
- Location of Alignment in SEQ ID NO 2612: from 1 to 109
- Alignment No. 15811
- gi No. 2464957
- % Identity 89.5
- Alignment Length 86
- Location of Alignment in SEQ ID NO 2612: from 25 to 109
- Alignment No. 15812
- gi No. 249170
- % Identity 92.3
- Alignment Length 39
- Location of Alignment in SEQ ID NO 2612: from 1 to 34
- Alignment No. 15813
- gi No. 249171
- % Identity 75.4
- Alignment Length 61
- Location of Alignment in SEQ ID NO 2612: from 41 to 97
- Alignment No. 15814
- gi No. 254773
- % Identity 100
- Alignment Length 20
- Location of Alignment in SEQ ID NO 2612: from 72 to 91
- Alignment No. 15815
- gi No. 2554673
- % Identity 93.3
- Alignment Length 75
- Location of Alignment in SEQ ID NO 2612: from 1 to 40
- Alignment No. 15816
- gi No. 2623680
- % Identity 98.6
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2612: from 1 to 109
- Alignment No. 15817

- gi No. 2654179
- % Identity 93
- Alignment Length 86
- Location of Alignment in SEQ ID NO 2612: from 2 to 87
- Alignment No. 15818
- gi No. 266018
- % Identity 91.2
- Alignment Length 34
- Location of Alignment in SEQ ID NO 2612: from 60 to 93
- Alignment No. 15819
- gi No. 2677834
- % Identity 93.6
- Alignment Length 110
- Location of Alignment in SEQ ID NO 2612: from 1 to 93
- Alignment No. 15820
- gi No. 2809481
- % Identity 98.6
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2612: from 1 to 109
- Alignment No. 15821
- qi No. 2832598
- % Identity 91.8
- Alignment Length 134
- Location of Alignment in SEQ ID NO 2612: from 1 to 105
- Alignment No. 15822
- gi No. 289525
- % Identity 98.6
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2612: from 1 to 109
- Alignment No. 15823
- gi No. 2959326
- % Identity 71.7
- Alignment Length 130
- Location of Alignment in SEQ ID NO 2612: from 1 to 93
- Alignment No. 15824
- gi No. 3021331
- % Identity 83.8
- Alignment Length 68
- Location of Alignment in SEQ ID NO 2612: from 38 to 105
- Alignment No. 15825
- gi No. 310563
- % Identity 78.8
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2612: from 1 to 109
- Alignment No. 15826
- gi No. 3121848
- % Identity 98.6
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2612: from 1 to 109
- Alignment No. 15827
- gi No. 3121849

- % Identity 98.6
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2612: from 1 to 109
- Alignment No. 15828
- gi No. 3136336
- % Identity 98.6
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2612: from 1 to 109
- Alignment No. 15829
- gi No. 3243222
- % Identity 88.6
- Alignment Length 35
- Location of Alignment in SEQ ID NO 2612: from 41 to 75
- Alignment No. 15830
- gi No. 3336912
- % Identity 93.8
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2612: from 1 to 109
- Alignment No. 15831
- gi No. 3378652
- % Identity 100
- Alignment Length 119
- Location of Alignment in SEQ ID NO 2612: from 1 to 109
- Alignment No. 15832
- gi No. 3415119
- % Identity 89.7
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2612: from 1 to 109
- Alignment No. 15833
- gi No. 348265
- % Identity 100
- Alignment Length 29
- Location of Alignment in SEQ ID NO 2612: from 1 to 24
- Alignment No. 15834
- gi No. 348267
- % Identity 94.7
- Alignment Length 19
- Location of Alignment in SEQ ID NO 2612: from 72 to 90
- Alignment No. 15835
- qi No. 348268
- % Identity 78.9
- Alignment Length 19
- Location of Alignment in SEQ ID NO 2612: from 92 to 109
- Alignment No. 15836
- qi No. 3561059
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2612: from 1 to 109
- Alignment No. 15837
- gi No. 3561061
- % Identity 95.9



- Alignment Length 146
- Location of Alignment in SEQ ID NO 2612: from 1 to 109
- Alignment No. 15838
- gi No. 3786339
- % Identity 91.1
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2612: from 1 to 109
- Alignment No. 15839
- gi No. 3800845
- % Identity 82.2
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2612: from 1 to 109
- Alignment No. 15840
- gi No. 3800847
- % Identity 74.7
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2612: from 1 to 109
- Alignment No. 15841
- gi No. 3800849
- % Identity 87.7
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2612: from 1 to 109
- Alignment No. 15842
- gi No. 3800851
- % Identity 72.6
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2612: from 1 to 109
- Alignment No. 15843
- gi No. 3913191
- % Identity 97.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2612: from 1 to 109
- Alignment No. 15844
- gi No. 4028590
- % Identity 82.2
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2612: from 1 to 109
- Alignment No. 15845
- gi No. 4033343
- % Identity 82.1
- Alignment Length 145
- Location of Alignment in SEQ ID NO 2612: from 1 to 109
- Alignment No. 15846
- gi No. 4033509
- % Identity 90.4
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2612: from 1 to 109
- Alignment No. 15847
- qi No. 4098293
- % Identity 95.3
- Alignment Length 107



- Location of Alignment in SEQ ID NO 2612: from 1 to 90
- Alignment No. 15848
- gi No. 4098295
- % Identity 86
- Alignment Length 107
- Location of Alignment in SEQ ID NO 2612: from 1 to 90
- Alignment No. 15849
- gi No. 4103778
- % Identity 94.1
- Alignment Length 17
- Location of Alignment in SEQ ID NO 2612: from 94 to 109
- Alignment No. 15850
- gi No. 4103959
- % Identity 97.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2612: from 1 to 109
- Alignment No. 15851
- gi No. 4103963
- % Identity 100
- Alignment Length 65
- Location of Alignment in SEQ ID NO 2612: from 46 to 109
- Alignment No. 15852
- gi No. 4103965

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- % Identity 100
- Alignment Length 64
- Location of Alignment in SEQ ID NO 2612: from 47 to 109
- Alignment No. 15853
- gi No. 4150908
- % Identity 90.4
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2612: from 1 to 109
- Alignment No. 15854
- gi No. 4200039
- % Identity 88.4
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2612: from 1 to 109
- Alignment No. 15855
- gi No. 4335787
- % Identity 90.4
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2612: from 1 to 109
- Alignment No. 15856
- gi No. 4336136
- % Identity 87.2
- Alignment Length 47
- Location of Alignment in SEQ ID NO 2612: from 1 to 31
- Alignment No. 15857
- gi No. 4379369
- % Identity 93.2
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2612: from 1 to 109

- Alignment No. 15858
- gi No. 443167
- % Identity 87.6
- Alignment Length 145
- Location of Alignment in SEQ ID NO 2612: from 1 to 109
- Alignment No. 15859
- gi No. 4468115
- % Identity 91.1
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2612: from 1 to 109
- Alignment No. 15860
- gi No. 4502549
- % Identity 91.1
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2612: from 1 to 109
- Alignment No. 15861
- gi No. 4581211
- % Identity 87
- Alignment Length 77
- Location of Alignment in SEQ ID NO 2612: from 34 to 109
- Alignment No. 15862
- gi No. 4581213
- % Identity 78.1
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2612: from 1 to 109
- Alignment No. 15863
- gi No. 4585219
- % Identity 82.2
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2612: from 1 to 109
- Alignment No. 15864
- gi No. 461684
- % Identity 85.1
- Alignment Length 148
- Location of Alignment in SEQ ID NO 2612: from 1 to 109
- Alignment No. 15865
- gi No. 476851
- % Identity 85.7
- Alignment Length 77
- Location of Alignment in SEQ ID NO 2612: from 34 to 109
- Alignment No. 15866
- gi No. 484660
- % Identity 82.4
- Alignment Length 142
- Location of Alignment in SEQ ID NO 2612: from 1 to 108
- Alignment No. 15867
- gi No. 4885109
- % Identity 89.3
- Alignment Length 149
- Location of Alignment in SEQ ID NO 2612: from 1 to 109

- Alignment No. 15868
- gi No. 4885111
- % Identity 82.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2612: from 1 to 109
- Alignment No. 15869
- gi No. 4930156
- % Identity 95.9
- Alignment Length 145
- Location of Alignment in SEQ ID NO 2612: from 1 to 109
- Alignment No. 15870
- gi No. 4959142
- % Identity 94.5
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2612: from 1 to 109
- Alignment No. 15871
- gi No. 4959143
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2612: from 1 to 109
- Alignment No. 15872
- gi No. 4959144
- % Identity 95.2
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2612: from 1 to 109
- Alignment No. 15873
- gi No. 4959145
- % Identity 97.3
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2612: from 1 to 109
- Alignment No. 15874
- gi No. 4959146
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2612: from 1 to 109
- Alignment No. 15875
- gi No. 4959147
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2612: from 1 to 109
- Alignment No. 15876
- gi No. 4959148
- % Identity 94
- Alignment Length 149
- Location of Alignment in SEQ ID NO 2612: from 1 to 109
- Alignment No. 15877
- gi No. 4959149
- % Identity 95.2
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2612: from 1 to 109
- Alignment No. 15878

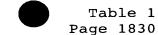
- gi No. 4959150
- % Identity 95.2
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2612: from 1 to 109
- Alignment No. 15879
- gi No. 4959151
- % Identity 95.2
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2612: from 1 to 109
- Alignment No. 15880
- gi No. 4959152
- % Identity 93.2
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2612: from 1 to 109
- Alignment No. 15881
- gi No. 4959153
- % Identity 93.2
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2612: from 1 to 109
- Alignment No. 15882
- gi No. 4959154
- % Identity 92.5
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2612: from 1 to 109
- Alignment No. 15883
- gi No. 4959155
- % Identity 92.5
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2612: from 1 to 109
- Alignment No. 15884
- gi No. 4959156
- % Identity 93.2
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2612: from 1 to 109
- Alignment No. 15885
- gi No. 4959157
- % Identity 91.8
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2612: from 1 to 109
- Alignment No. 15886
- gi No. 4959159
- % Identity 89
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2612: from 1 to 109
- Alignment No. 15887
- gi No. 4959160
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2612: from 1 to 109
- Alignment No. 15888
- gi No. 4959161

- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2612: from 1 to 109
- Alignment No. 15889
- qi No. 4959162
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2612: from 1 to 109
- Alignment No. 15890
- gi No. 4959163
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2612: from 1 to 109
- Alignment No. 15891
- qi No. 4959164
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2612: from 1 to 109
- Alignment No. 15892
- gi No. 4959165
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2612: from 1 to 109
- Alignment No. 15893
- gi No. 4959166
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2612: from 1 to 109
- Alignment No. 15894
- gi No. 4959167
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2612: from 1 to 109
- Alignment No. 15895
- gi No. 4959168
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID.NO 2612: from 1 to 109
- Alignment No. 15896
- gi No. 4959169
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2612: from 1 to 109
- Alignment No. 15897
- qi No. 4959170
- % Identity 95.2
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2612: from 1 to 109
- Alignment No. 15898
- gi No. 4959171
- % Identity 95.9

- Alignment Length 146
- Location of Alignment in SEQ ID NO 2612: from 1 to 109
- Alignment No. 15899
- gi No. 4959172
- % Identity 96.6
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2612: from 1 to 109
- Alignment No. 15900
- gi No. 4959588
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2612: from 1 to 109
- Alignment No. 15901
- gi No. 4959590
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2612: from 1 to 109
- Alignment No. 15902
- gi No. 4959593
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2612: from 1 to 109
- Alignment No. 15903
- gi No. 4959594
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2612: from 1 to 109
- Alignment No. 15904
- gi No. 4959598
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2612: from 1 to 109
- Alignment No. 15905
- gi No. 4959599
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2612: from 1 to 109
- Alignment No. 15906
- gi No. 4959600
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2612: from 1 to 109
- Alignment No. 15907
- gi No. 4959602
- % Identity 94.5
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2612: from 1 to 109
- Alignment No. 15908
- gi No. 4959604
- % Identity 95.9
- Alignment Length 146

"]

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- Location of Alignment in SEQ ID NO 2612: from 1 to 109
- Alignment No. 15909
- gi No. 4959612
- % Identity 93.8
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2612: from 1 to 109
- Alignment No. 15910
- gi No. 4959613
- % Identity 91.8
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2612: from 1 to 109
- Alignment No. 15911
- gi No. 4959614
- % Identity 95.2
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2612: from 1 to 109
- Alignment No. 15912
- gi No. 4959615
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2612: from 1 to 109 $\,$
- Alignment No. 15913
- gi No. 4959616
- % Identity 94.5
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2612: from 1 to 109
- Alignment No. 15914
- gi No. 4959617
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2612: from 1 to 109
- Alignment No. 15915
- gi No. 4959618
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2612: from 1 to 109
- Alignment No. 15916
- gi No. 4959621
- % Identity 94.5
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2612: from 1 to 109
- Alignment No. 15917
- gi No. 4959622
- % Identity 92.5
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2612: from 1 to 109
- Alignment No. 15918
- gi No. 4959625
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2612: from 1 to 109

- Alignment No. 15919 - gi No. 4959626 - % Identity 95.9 - Alignment Length 146 - Location of Alignment in SEQ ID NO 2612: from 1 to 109 - Alignment No. 15920 - gi No. 4959629 - % Identity 94.6 - Alignment Length 149 - Location of Alignment in SEQ ID NO 2612: from 1 to 109 - Alignment No. 15921 - gi No. 4959630 - % Identity 95.2 - Alignment Length 146 - Location of Alignment in SEQ ID NO 2612: from 1 to 109 - Alignment No. 15922 - gi No. 4959635 - % Identity 95.9 - Alignment Length 146 - Location of Alignment in SEQ ID NO 2612: from 1 to 109 - Alignment No. 15923 - gi No. 4959636 - % Identity 95.9 - Alignment Length 146 - Location of Alignment in SEQ ID NO 2612: from 1 to 109 - Alignment No. 15924 - gi No. 4959637 - % Identity 95.9 - Alignment Length 146 - Location of Alignment in SEQ ID NO 2612: from 1 to 109 - Alignment No. 15925 - gi No. 4959638 - % Identity 95.9 - Alignment Length 146 - Location of Alignment in SEQ ID NO 2612: from 1 to 109 - Alignment No. 15926 - gi No. 4959640 - % Identity 95.9 - Alignment Length 146 - Location of Alignment in SEQ ID NO 2612: from 1 to 109 - Alignment No. 15927 - gi No. 4959645 - % Identity 95.9 - Alignment Length 146 - Location of Alignment in SEQ ID NO 2612: from 1 to 109 - Alignment No. 15928 - gi No. 4959646 - % Identity 96.6 - Alignment Length 146 - Location of Alignment in SEQ ID NO 2612: from 1 to 109

- Alignment No. 15929
- gi No. 4959647
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2612: from 1 to 109
- Alignment No. 15930
- gi No. 4959648
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2612: from 1 to 109
- Alignment No. 15931
- gi No. 4995673
- % Identity 100 Alignment Length 22
- Location of Alignment in SEQ ID NO 2612: from 13 to 34
- Alignment No. 15932
- gi No. 4995696
- % Identity 95.5
- Alignment Length 22
- Location of Alignment in SEQ ID NO 2612: from 13 to 34
- Alignment No. 15933
- gi No. 4995737
- % Identity 82.6
- Alignment Length 23
- Location of Alignment in SEQ ID NO 2612: from 13 to 35
- Alignment No. 15934
- gi No. 4995739
- % Identity 91.3
- Alignment Length 23
- Location of Alignment in SEQ ID NO 2612: from 13 to 35
- Alignment No. 15935
- gi No. 508526
- % Identity 90.8
- Alignment Length 131
- Location of Alignment in SEQ ID NO 2612: from 1 to 95
- Alignment No. 15936
- gi No. 535428
- % Identity 76
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2612: from 1 to 109
- Alignment No. 15937
- gi No. 552252
- % Identity 84.6
- Alignment Length 26
- Location of Alignment in SEQ ID NO 2612: from 39 to 64
- Alignment No. 15938
- qi No. 5640002
- % Identity 91.3
- Alignment Length 80
- Location of Alignment in SEQ ID NO 2612: from 25 to 104
- Alignment No. 15939

- gi No. 565166
- % Identity 86.2
- Alignment Length 145
- Location of Alignment in SEQ ID NO 2612: from 1 to 109
- Alignment No. 15940
- gi No. 576081
- % Identity 89.4
- Alignment Length 141
- Location of Alignment in SEQ ID NO 2612: from 1 to 109
- Alignment No. 15941
- gi No. 587454
- % Identity 90.5
- Alignment Length 137
- Location of Alignment in SEQ ID NO 2612: from 1 to 109
- Alignment No. 15942
- gi No. 640285
- % Identity 91
- Alignment Length 145
- Location of Alignment in SEQ ID NO 2612: from 1 to 109
- Alignment No. 15943
- gi No. 640294
- % Identity 90.8
- Alignment Length 142
- Location of Alignment in SEQ ID NO 2612: from 1 to 109
- Alignment No. 15944
- gi No. 71660
- % Identity 90.3
- Alignment Length 145
- Location of Alignment in SEQ ID NO 2612: from 1 to 109
- Alignment No. 15945
- gi No. 71662
- % Identity 91
- Alignment Length 145
- Location of Alignment in SEQ ID NO 2612: from 1 to 109
- Alignment No. 15946
- gi No. 71667
- % Identity 91.7
- Alignment Length 145
- Location of Alignment in SEQ ID NO 2612: from 1 to 109
- Alignment No. 15947
- gi No. 71673
- % Identity 90.3
- Alignment Length 145
- Location of Alignment in SEQ ID NO 2612: from 1 to 109
- Alignment No. 15948
- gi No. 71676
- % Identity 84.8
- Alignment Length 145
- Location of Alignment in SEQ ID NO 2612: from 1 to 109
- Alignment No. 15949
- gi No. 729010

- % Identity 98.6
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2612: from 1 to 109
- Alignment No. 15950
- gi No. 729011
- % Identity 82.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2612: from 1 to 109
- Alignment No. 15951
- gi No. 729012
- % Identity 87.3
- Alignment Length 142
- Location of Alignment in SEQ ID NO 2612: from 1 to 109
- Alignment No. 15952
- gi No. 809298
- % Identity 86.9
- Alignment Length 145
- Location of Alignment in SEQ ID NO 2612: from 1 to 109
- Alignment No. 15953
- gi No. 85332
- % Identity 92.2
- Alignment Length 141
- Location of Alignment in SEQ ID NO 2612: from 1 to 106 $\,$
- Alignment No. 15954
- gi No. 9874
- % Identity 85.6
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2612: from 1 to 109
- Alignment No. 15955
- gi No. 99673
- % Identity 81.9
- Alignment Length 72
- Location of Alignment in SEQ ID NO 2612: from 1 to 38
- (B) Polypeptide Sequence
 - Pat. Appln. SEQ ID NO 2613
 - Ceres seq_id 1503992
 - Location of start within SEQ ID NO 2610: at 220 nt.
- (C) Nomination and Annotation of Domains within Predicted Polypeptide(s) $% \left(1\right) =\left(1\right) \left(1\right) +\left(1\right) \left(1\right) \left(1\right) +\left(1\right) \left(1\right)$
 - Alignment No. 15956
 - EF hand
 - Location within SEQ ID NO 2613: from 1 to 25 aa.
 - (D) Related Amino Acid Sequences
 - Alignment No. 15957
 - gi No. 100665
 - % Identity 99.3
 - Alignment Length 146
 - Location of Alignment in SEQ ID NO 2613: from 1 to 94
 - Alignment No. 15958
 - gi No. 1076792
 - % Identity 97.9

- Alignment Length 146
- Location of Alignment in SEQ ID NO 2613: from 1 to 94
- Alignment No. 15959
- gi No. 1076793
- % Identity 98.6
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2613: from 1 to 94
- Alignment No. 15960
- gi No. 1084453
- % Identity 98.6
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2613: from 1 to 94
- Alignment No. 15961
- gi No. 1085679
- % Identity 91.8
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2613: from 1 to 94
- Alignment No. 15962
- gi No. 115480
- % Identity 97.7
- Alignment Length 133
- Location of Alignment in SEQ ID NO 2613: from 1 to 94
- Alignment No. 15963
- gi No. 115484
- % Identity 99.3
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2613: from 1 to 94
- Alignment No. 15964
- gi No. 115486
- % Identity 98.6
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2613: from 1 to 94
- Alignment No. 15965
- gi No. 115489
- % Identity 91.1
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2613: from 1 to 94
- Alignment No. 15966
- gi No. 115492
- % Identity 99.3
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2613: from 1 to 94
- Alignment No. 15967
- gi No. 115500
- % Identity 91.9
- Alignment Length 135
- Location of Alignment in SEQ ID NO 2613: from 1 to 94
- Alignment No. 15968
- gi No. 115503
- % Identity 89.7
- Alignment Length 146

- Location of Alignment in SEQ ID NO 2613: from 1 to 94
- Alignment No. 15969
- gi No. 115504
- % Identity 82.2
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2613: from 1 to 94
- Alignment No. 15970
- gi No. 115506
- % Identity 87.5
- Alignment Length 144
- Location of Alignment in SEQ ID NO 2613: from 1 to 94
- Alignment No. 15971
- gi No. 115508
- % Identity 91.8
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2613: from 1 to 94
- Alignment No. 15972
- gi No. 115509
- % Identity 90.4
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2613: from 1 to 94
- Alignment No. 15973
- gi No. 115510
- % Identity 90.3
- Alignment Length 145
- Location of Alignment in SEQ ID NO 2613: from 1 to 94
- Alignment No. 15974
- gi No. 115511
- % Identity 100
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2613: from 1 to 94
- Alignment No. 15975
- gi No. 115513
- % Identity 93.2
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2613: from 1 to 94 $\,$
- Alignment No. 15976
- gi No. 115514
- % Identity 80
- Alignment Length 30
- Location of Alignment in SEQ ID NO 2613: from 24 to 53
- Alignment No. 15977
- gi No. 115515
- % Identity 98.6
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2613: from 1 to 94
- Alignment No. 15978
- gi No. 115516
- % Identity 91
- Alignment Length 145
- Location of Alignment in SEQ ID NO 2613: from 1 to 94

- gi No. 115527
- % Identity 87
- Alignment Length 77

- Alignment No. 15979 - gi No. 115518 - % Identity 90.3 - Alignment Length 145 - Location of Alignment in SEQ ID NO 2613: from 1 to 94 - Alignment No. 15980 - gi No. 115519 - % Identity 91.8 - Alignment Length 146 - Location of Alignment in SEQ ID NO 2613: from 1 to 94 - Alignment No. 15981 - gi No. 115520 - % Identity 87 - Alignment Length 146 - Location of Alignment in SEQ ID NO 2613: from 1 to 94 - Alignment No. 15982 - gi No. 115521 - % Identity 89.7 - Alignment Length 145 - Location of Alignment in SEQ ID NO 2613: from 1 to 94 - Alignment No. 15983 - gi No. 115522 - % Identity 91 - Alignment Length 145 - Location of Alignment in SEQ ID NO 2613: from 1 to 94 - Alignment No. 15984 - gi No. 115523 - % Identity 75.4 - Alignment Length 142 - Location of Alignment in SEQ ID NO 2613: from 1 to 94 - Alignment No. 15985 - gi No. 115524 - % Identity 92.5 - Alignment Length 146 - Location of Alignment in SEQ ID NO 2613: from 1 to 94 - Alignment No. 15986 - gi No. 115525 - % Identity 97.9 - Alignment Length 145 - Location of Alignment in SEQ ID NO 2613: from 1 to 94 - Alignment No. 15987 - qi No. 115526 - % Identity 91 - Alignment Length 145 - Location of Alignment in SEQ ID NO 2613: from 1 to 94 - Alignment No. 15988

- Location of Alignment in SEQ ID NO 2613: from 19 to 94

- Alignment No. 15989 - gi No. 115528 - % Identity 90.4 - Alignment Length 146 - Location of Alignment in SEQ ID NO 2613: from 1 to 94 - Alignment No. 15990 - qi No. 115530 - % Identity 90.4 - Alignment Length 146 - Location of Alignment in SEQ ID NO 2613: from 1 to 94 - Alignment No. 15991 - gi No. 115531 - % Identity 91.1 - Alignment Length 146 - Location of Alignment in SEQ ID NO 2613: from 1 to 94 - Alignment No. 15992 - gi No. 115532 - % Identity 97.9 - Alignment Length 146 - Location of Alignment in SEQ ID NO 2613: from 1 to 94 - Alignment No. 15993 - gi No. 115534 - % Identity 93.1 - Alignment Length 131 - Location of Alignment in SEQ ID NO 2613: from 1 to 91 - Alignment No. 15994 - gi No. 115541 - % Identity 83.6 - Alignment Length 146 - Location of Alignment in SEQ ID NO 2613: from 1 to 94 - Alignment No. 15995 - gi No. 1168748 - % Identity 95.9 - Alignment Length 146 - Location of Alignment in SEQ ID NO 2613: from 1 to 94 - Alignment No. 15996 - gi No. 1168749 - % Identity 98.6 - Alignment Length 146 - Location of Alignment in SEQ ID NO 2613: from 1 to 94 - Alignment No. 15997 - gi No. 1235664 - % Identity 85.6 - Alignment Length 146 - Location of Alignment in SEQ ID NO 2613: from 1 to 94
- Alignment No. 15998
- gi No. 1292710
- % Identity 97.3
- Alignment Length 147
- Location of Alignment in SEQ ID NO 2613: from 1 to 94
- Alignment No. 15999

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Table 1

- gi No. 1292853
- % Identity 88.4
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2613: from 1 to 94
- Alignment No. 16000
- gi No. 1311052
- % Identity 88.6
- Alignment Length 70
- Location of Alignment in SEQ ID NO 2613: from 26 to 94
- Alignment No. 16001
- gi No. 1345660
- % Identity 98.6
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2613: from 1 to 94
- Alignment No. 16002
- qi No. 1345661
- % Identity 87.7
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2613: from 1 to 94
- Alignment No. 16003
- gi No. 1362058
- % Identity 96.6
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2613: from 1 to 94
- Alignment No. 16004
- gi No. 1402947
- % Identity 97.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2613: from 1 to 94
- Alignment No. 16005
- gi No. 1421816
- % Identity 85.5
- Alignment Length 145
- Location of Alignment in SEQ ID NO 2613: from 1 to 94
- Alignment No. 16006
- gi No. 1565285
- % Identity 93.2
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2613: from 1 to 94
- Alignment No. 16007
- gi No. 162030
- % Identity 89.7
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2613: from 1 to 94
- Alignment No. 16008
- gi No. 16225
- % Identity 99.3
- Alignment Length 135
- Location of Alignment in SEQ ID NO 2613: from 1 to 94
- Alignment No. 16009
- gi No. 166655

- % Identity 98.6
- Alignment Length 140
- Location of Alignment in SEQ ID NO 2613: from 1 to 94
- Alignment No. 16010
- gi No. 167676
- % Identity 87.4
- Alignment Length 135
- Location of Alignment in SEQ ID NO 2613: from 1 to 94
- Alignment No. 16011
- gi No. 168777
- % Identity 82.2
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2613: from 1 to 94
- Alignment No. 16012
- gi No. 169406
- % Identity 88
- Alignment Length 75
- Location of Alignment in SEQ ID NO 2613: from 1 to 64
- Alignment No. 16013
- gi No. 170076
- % Identity 79.5
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2613: from 1 to 94
- Alignment No. 16014
- gi No. 1705567
- % Identity 85.4
- Alignment Length 144
- Location of Alignment in SEQ ID NO 2613: from 1 to 94
- Alignment No. 16015
- gi No. 1754997
- % Identity 98.3
- Alignment Length 121
- Location of Alignment in SEQ ID NO 2613: from 1 to 94
- Alignment No. 16016
- gi No. 1754999
- % Identity 98.6
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2613: from 1 to 94
- Alignment No. 16017
- gi No. 1785953
- % Identity 84.1
- Alignment Length 63
- Location of Alignment in SEQ ID NO 2613: from 6 to 68
- Alignment No. 16018
- gi No. 1785955
- % Identity 72.5
- Alignment Length 131
- Location of Alignment in SEQ ID NO 2613: from 1 to 94
- Alignment No. 16019
- gi No. 1785958
- % Identity 87.3

- Alignment Length 63
- Location of Alignment in SEQ ID NO 2613: from 6 to 68
- Alignment No. 16020
- gi No. 20186
- % Identity 99.3
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2613: from 1 to 94
- Alignment No. 16021
- gi No. 208092
- % Identity 96.6
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2613: from 1 to 94
- Alignment No. 16022
- gi No. 2119350
- % Identity 92.2
- Alignment Length 51
- Location of Alignment in SEQ ID NO 2613: from 26 to 76
- Alignment No. 16023
- gi No. 2119353
- % Identity 91.8
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2613: from 1 to 94
- Alignment No. 16024
- gi No. 2119360
- % Identity 99.2
- Alignment Length 121
- Location of Alignment in SEQ ID NO 2613: from 1 to 94
- Alignment No. 16025
- gi No. 2119361
- % Identity 94.2
- Alignment Length 121
- Location of Alignment in SEQ ID NO 2613: from 1 to 94
- Alignment No. 16026
- gi No. 2119362
- % Identity 90.4
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2613: from 1 to 94
- Alignment No. 16027
- gi No. 2119364
- % Identity 90
- Alignment Length 20
- Location of Alignment in SEQ ID NO 2613: from 43 to 62
- Alignment No. 16028
- gi No. 2129978
- % Identity 97.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2613: from 1 to 94
- Alignment No. 16029
- gi No. 2147165
- % Identity 98.6
- Alignment Length 146

- Location of Alignment in SEQ ID NO 2613: from 1 to 94 - Alignment No. 16030 - gi No. 2181205 - % Identity 92.5 - Alignment Length 146 - Location of Alignment in SEQ ID NO 2613: from 1 to 94 - Alignment No. 16031 - gi No. 222925 - % Identity 92.6 - Alignment Length 136 - Location of Alignment in SEQ ID NO 2613: from 1 to 92 - Alignment No. 16032 - gi No. 223036 - % Identity 88.3 - Alignment Length 145 - Location of Alignment in SEQ ID NO 2613: from 1 to 94 - Alignment No. 16033 - gi No. 223218 - % Identity 89 - Alignment Length 145 - Location of Alignment in SEQ ID NO 2613: from 1 to 94 - Alignment No. 16034 - gi No. 223872 - % Identity 86.9 - Alignment Length 145 - Location of Alignment in SEQ ID NO 2613: from 1 to 94 - Alignment No. 16035 - gi No. 2244820 - % Identity 75.4 - Alignment Length 142 - Location of Alignment in SEQ ID NO 2613: from 1 to 94 - Alignment No. 16036 - gi No. 225024 - % Identity 87.5 - Alignment Length 144 - Location of Alignment in SEQ ID NO 2613: from 1 to 94 - Alignment No. 16037 - gi No. 2267084 - % Identity 94.1 - Alignment Length 135 - Location of Alignment in SEQ ID NO 2613: from 1 to 94 - Alignment No. 16038 - gi No. 228408 - % Identity 97.7 - Alignment Length 133 - Location of Alignment in SEQ ID NO 2613: from 1 to 94 - Alignment No. 16039 - gi No. 2291247 - % Identity 91.8 - Alignment Length 146

- Location of Alignment in SEQ ID NO 2613: from 1 to 94

- Alignment No. 16040
- gi No. 230381
- % Identity 88.2
- Alignment Length 68
- Location of Alignment in SEQ ID NO 2613: from 28 to 94
- Alignment No. 16041
- gi No. 230382
- % Identity 86.4
- Alignment Length 66
- Location of Alignment in SEQ ID NO 2613: from 30 to 94
- Alignment No. 16042
- gi No. 2388889
- % Identity 99.2
- Alignment Length 118
- Location of Alignment in SEQ ID NO 2613: from 1 to 75
- Alignment No. 16043
- gi No. 2388891
- % Identity 95.2
- Alignment Length 104
- Location of Alignment in SEQ ID NO 2613: from 1 to 53
- Alignment No. 16044
- gi No. 2392137
- % Identity 90.3
- Alignment Length 145
- Location of Alignment in SEQ ID NO 2613: from 1 to 94
- Alignment No. 16045
- gi No. 2464957
- % Identity 89.5
- Alignment Length 86
- Location of Alignment in SEQ ID NO 2613: from 10 to 94
- Alignment No. 16046
- gi No. 249170
- % Identity 92.3
- Alignment Length 39
- Location of Alignment in SEQ ID NO 2613: from 1 to 19
- Alignment No. 16047
- gi No. 249171
- % Identity 75.4
- Alignment Length 61
- Location of Alignment in SEQ ID NO 2613: from 26 to 82
- Alignment No. 16048
- gi No. 254773
- % Identity 100
- Alignment Length 20
- Location of Alignment in SEQ ID NO 2613: from 57 to 76
- Alignment No. 16049
- gi No. 2554673
- % Identity 93.3
- Alignment Length 75
- Location of Alignment in SEQ ID NO 2613: from 1 to 25

- Alignment No. 16050 - gi No. 2623680 - % Identity 98.6 - Alignment Length 146 - Location of Alignment in SEQ ID NO 2613: from 1 to 94 - Alignment No. 16051 - gi No. 2654179 - % Identity 93 - Alignment Length 86 - Location of Alignment in SEQ ID NO 2613: from 1 to 72 - Alignment No. 16052 - gi No. 266018 - % Identity 91.2 - Alignment Length 34 - Location of Alignment in SEQ ID NO 2613: from 45 to 78 - Alignment No. 16053 - gi No. 2677834 - % Identity 93.6 - Alignment Length 110 - Location of Alignment in SEQ ID NO 2613: from 1 to 78 - Alignment No. 16054 - gi No. 2809481 - % Identity 98.6 - Alignment Length 146 - Location of Alignment in SEQ ID NO 2613: from 1 to 94 - Alignment No. 16055 - gi No. 2832598 - % Identity 91.8 - Alignment Length 134 - Location of Alignment in SEQ ID NO 2613: from 1 to 90 - Alignment No. 16056 - qi No. 289525 - % Identity 98.6 - Alignment Length 146 - Location of Alignment in SEQ ID NO 2613: from 1 to 94 - Alignment No. 16057 - gi No. 2959326 - % Identity 71.7 - Alignment Length 130 - Location of Alignment in SEQ ID NO 2613: from 1 to 78 - Alignment No. 16058 - gi No. 3021331
- Alignment No. 16059
- gi No. 310563
- % Identity 78.8

% Identity 83.8Alignment Length 68

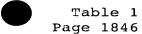
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2613: from 1 to 94

- Location of Alignment in SEQ ID NO 2613: from 23 to 90

- Alignment No. 16060

- gi No. 3121848
- % Identity 98.6
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2613: from 1 to 94
- Alignment No. 16061
- gi No. 3121849
- % Identity 98.6
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2613: from 1 to 94
- Alignment No. 16062
- gi No. 3136336
- % Identity 98.6
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2613: from 1 to 94
- Alignment No. 16063
- gi No. 3243222
- % Identity 88.6
- Alignment Length 35
- Location of Alignment in SEQ ID NO 2613: from 26 to 60
- Alignment No. 16064
- gi No. 3336912
- % Identity 93.8
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2613: from 1 to 94
- Alignment No. 16065
- gi No. 3378652
- % Identity 100
- Alignment Length 119
- Location of Alignment in SEQ ID NO 2613: from 1 to 94
- Alignment No. 16066
- gi No. 3415119
- % Identity 89.7
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2613: from 1 to 94
- Alignment No. 16067
- gi No. 348267
- % Identity 94.7
- Alignment Length 19
- Location of Alignment in SEQ ID NO 2613: from 57 to 75
- Alignment No. 16068
- gi No. 348268
- % Identity 78.9
- Alignment Length 19
- Location of Alignment in SEQ ID NO 2613: from 77 to 94
- Alignment No. 16069
- gi No. 3561059
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2613: from 1 to 94
- Alignment No. 16070
- gi No. 3561061

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- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2613: from 1 to 94
- Alignment No. 16071
- gi No. 3786339
- % Identity 91.1
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2613: from 1 to 94
- Alignment No. 16072
- gi No. 3800845
- % Identity 82.2
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2613: from 1 to 94
- Alignment No. 16073
- qi No. 3800847
- % Identity 74.7
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2613: from 1 to 94
- Alignment No. 16074
- gi No. 3800849
- % Identity 87.7
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2613: from 1 to 94
- Alignment No. 16075
- gi No. 3800851
- % Identity 72.6
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2613: from 1 to 94
- Alignment No. 16076
- gi No. 3913191
- % Identity 97.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2613: from 1 to 94
- Alignment No. 16077
- gi No. 4028590
- % Identity 82.2
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2613: from 1 to 94
- Alignment No. 16078
- gi No. 4033343
- % Identity 82.1
- Alignment Length 145
- Location of Alignment in SEQ ID NO 2613: from 1 to 94
- Alignment No. 16079
- gi No. 4033509
- % Identity 90.4
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2613: from 1 to 94
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- Alignment No. 16080
- gi No. 4098293
- % Identity 95.3

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- Alignment Length 107
- Location of Alignment in SEQ ID NO 2613: from 1 to 75
- Alignment No. 16081
- gi No. 4098295
- % Identity 86
- Alignment Length 107
- Location of Alignment in SEQ ID NO 2613: from 1 to 75
- Alignment No. 16082
- gi No. 4103778
- % Identity 94.1
- Alignment Length 17
- Location of Alignment in SEQ ID NO 2613: from 79 to 94
- Alignment No. 16083
- gi No. 4103959
- % Identity 97.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2613: from 1 to 94
- Alignment No. 16084
- gi No. 4103963
- % Identity 100
- Alignment Length 65
- Location of Alignment in SEQ ID NO 2613: from 31 to 94
- Alignment No. 16085
- gi No. 4103965
- % Identity 100
- Alignment Length 64
- Location of Alignment in SEQ ID NO 2613: from 32 to 94
- Alignment No. 16086
- gi No. 4150908
- % Identity 90.4
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2613: from 1 to 94
- Alignment No. 16087
- gi No. 4200039
- % Identity 88.4
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2613: from 1 to 94
- Alignment No. 16088
- gi No. 4335787
- % Identity 90.4
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2613: from 1 to 94
- Alignment No. 16089
- gi No. 4336136
- % Identity 87.2
- Alignment Length 47
- Location of Alignment in SEQ ID NO 2613: from 1 to 16
- Alignment No. 16090
- gi No. 4379369
- % Identity 93.2
- Alignment Length 146

- % Identity 87.6

- Page 1848 - Location of Alignment in SEQ ID NO 2613: from 1 to 94 - Alignment No. 16091 - gi No. 443167
- Alignment Length 145 - Location of Alignment in SEQ ID NO 2613: from 1 to 94
- Alignment No. 16092 - gi No. 4468115 - % Identity 91.1 - Alignment Length 146
- Location of Alignment in SEQ ID NO 2613: from 1 to 94
- Alignment No. 16093 - gi No. 4502549 - % Identity 91.1 - Alignment Length 146
- Location of Alignment in SEQ ID NO 2613: from 1 to 94
- Alignment No. 16094 - gi No. 4581211 - % Identity 87
- Alignment Length 77
- Location of Alignment in SEQ ID NO 2613: from 19 to 94
- Alignment No. 16095 - gi No. 4581213 - % Identity 78.1
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2613: from 1 to 94
- Alignment No. 16096
- gi No. 4585219
- % Identity 82.2
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2613: from 1 to 94
- Alignment No. 16097
- qi No. 461684
- % Identity 85.1
- Alignment Length 148
- Location of Alignment in SEQ ID NO 2613: from 1 to 94
- Alignment No. 16098
- gi No. 476851
- % Identity 85.7
- Alignment Length 77
- Location of Alignment in SEQ ID NO 2613: from 19 to 94
- Alignment No. 16099
- gi No. 484660
- % Identity 82.4
- Alignment Length 142
- Location of Alignment in SEQ ID NO 2613: from 1 to 93
- Alignment No. 16100
- gi No. 4885109
- % Identity 89.3
- Alignment Length 149
- Location of Alignment in SEQ ID NO 2613: from 1 to 94

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Table 1 Page 1849

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- Alignment No. 16101
- gi No. 4885111
- % Identity 82.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2613: from 1 to 94
- Alignment No. 16102
- gi No. 4930156
- % Identity 95.9
- Alignment Length 145
- Location of Alignment in SEQ ID NO 2613: from 1 to 94
- Alignment No. 16103
- gi No. 4959142
- % Identity 94.5
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2613: from 1 to 94
- Alignment No. 16104
- gi No. 4959143
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2613: from 1 to 94
- Alignment No. 16105
- gi No. 4959144
- % Identity 95.2
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2613: from 1 to 94
- Alignment No. 16106
- gi No. 4959145
- % Identity 97.3
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2613: from 1 to 94
- Alignment No. 16107
- gi No. 4959146
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2613: from 1 to 94
- Alignment No. 16108
- gi No. 4959147
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2613: from 1 to 94
- Alignment No. 16109
- gi No. 4959148
- % Identity 94
- Alignment Length 149
- Location of Alignment in SEQ ID NO 2613: from 1 to 94
- Alignment No. 16110
- gi No. 4959149
- % Identity 95.2
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2613: from 1 to 94
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- Alignment No. 16111 - gi No. 4959150 - % Identity 95.2 - Alignment Length 146 - Location of Alignment in SEQ ID NO 2613: from 1 to 94 - Alignment No. 16112 - gi No. 4959151 - % Identity 95.2 - Alignment Length 146 - Location of Alignment in SEQ ID NO 2613: from 1 to 94 - Alignment No. 16113 - gi No. 4959152 - % Identity 93.2 - Alignment Length 146 - Location of Alignment in SEQ ID NO 2613: from 1 to 94 - Alignment No. 16114 - gi No. 4959153 - % Identity 93.2 - Alignment Length 146 - Location of Alignment in SEQ ID NO 2613: from 1 to 94 - Alignment No. 16115 - gi No. 4959154 - % Identity 92.5 - Alignment Length 146 - Location of Alignment in SEQ ID NO 2613: from 1 to 94 - Alignment No. 16116 - gi No. 4959155 - % Identity 92.5 - Alignment Length 146 - Location of Alignment in SEQ ID NO 2613: from 1 to 94 - Alignment No. 16117 - gi No. 4959156 - % Identity 93.2 - Alignment Length 146 - Location of Alignment in SEQ ID NO 2613: from 1 to 94 - Alignment No. 16118 - gi No. 4959157 - % Identity 91.8 - Alignment Length 146 - Location of Alignment in SEQ ID NO 2613: from 1 to 94
- Alignment No. 16119
- gi No. 4959159
- % Identity 89
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2613: from 1 to 94
- Alignment No. 16120
- gi No. 4959160
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2613: from 1 to 94
- Alignment No. 16121

- gi No. 4959161 - % Identity 95.9 - Alignment Length 146 - Location of Alignment in SEQ ID NO 2613: from 1 to 94
- Alignment No. 16122 - gi No. 4959162 - % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2613: from 1 to 94
- Alignment No. 16123
- gi No. 4959163
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2613: from 1 to 94
- Alignment No. 16124
- gi No. 4959164
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2613: from 1 to 94
- Alignment No. 16125
- gi No. 4959165
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2613: from 1 to 94
- Alignment No. 16126
- gi No. 4959166
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2613: from 1 to 94
- Alignment No. 16127
- gi No. 4959167
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2613: from 1 to 94
- Alignment No. 16128
- gi No. 4959168
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2613: from 1 to 94
- Alignment No. 16129
- gi No. 4959169
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2613: from 1 to 94
- Alignment No. 16130
- gi No. 4959170
- % Identity 95.2
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2613: from 1 to 94
- Alignment No. 16131
- gi No. 4959171

- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2613: from 1 to 94
- Alignment No. 16132
- gi No. 4959172
- % Identity 96.6
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2613: from 1 to 94
- Alignment No. 16133
- gi No. 4959588
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2613: from 1 to 94
- Alignment No. 16134
- gi No. 4959590
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2613: from 1 to 94
- Alignment No. 16135
- gi No. 4959593
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2613: from 1 to 94
- Alignment No. 16136
- gi No. 4959594
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2613: from 1 to 94
- Alignment No. 16137
- gi No. 4959598
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2613: from 1 to 94
- Alignment No. 16138
- gi No. 4959599
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2613: from 1 to 94
- Alignment No. 16139
- gi No. 4959600
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2613: from 1 to 94
- Alignment No. 16140
- gi No. 4959602
- % Identity 94.5
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2613: from 1 to 94
- Alignment No. 16141
- gi No. 4959604
- % Identity 95.9

- Alignment Length 146
- Location of Alignment in SEQ ID NO 2613: from 1 to 94
- Alignment No. 16142
- gi No. 4959612
- % Identity 93.8
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2613: from 1 to 94
- Alignment No. 16143
- gi No. 4959613
- % Identity 91.8
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2613: from 1 to 94
- Alignment No. 16144
- gi No. 4959614
- % Identity 95.2
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2613: from 1 to 94
- Alignment No. 16145
- gi No. 4959615
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2613: from 1 to 94
- Alignment No. 16146
- gi No. 4959616
- % Identity 94.5
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2613: from 1 to 94
- Alignment No. 16147
- gi No. 4959617
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2613: from 1 to 94
- Alignment No. 16148
- gi No. 4959618
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2613: from 1 to 94
- Alignment No. 16149
- gi No. 4959621
- % Identity 94.5
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2613: from 1 to 94
- Alignment No. 16150
- gi No. 4959622
- % Identity 92.5
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2613: from 1 to 94
- Alignment No. 16151
- gi No. 4959625
- % Identity 95.9
- Alignment Length 146



- Location of Alignment in SEQ ID NO 2613: from 1 to 94
- Alignment No. 16152
- gi No. 4959626
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2613: from 1 to 94
- Alignment No. 16153
- gi No. 4959629
- % Identity 94.6
- Alignment Length 149
- Location of Alignment in SEQ ID NO 2613: from 1 to 94
- Alignment No. 16154
- gi No. 4959630
- % Identity 95.2
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2613: from 1 to 94
- Alignment No. 16155
- gi No. 4959635
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2613: from 1 to 94
- Alignment No. 16156
- gi No. 4959636
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2613: from 1 to 94
- Alignment No. 16157
- gi No. 4959637
- % Identity 95.9
- Alignment Length 146
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- Alignment No. 16158
- gi No. 4959638
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2613: from 1 to 94
- Alignment No. 16159
- qi No. 4959640
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2613: from 1 to 94
- Alignment No. 16160
- gi No. 4959645
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2613: from 1 to 94
- Alignment No. 16161
- qi No. 4959646
- % Identity 96.6
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2613: from 1 to 94

- Alignment No. 16162
- gi No. 4959647
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2613: from 1 to 94
- Alignment No. 16163
- gi No. 4959648
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2613: from 1 to 94
- Alignment No. 16164
- gi No. 4995673
- % Identity 100
- Alignment Length 22
- Location of Alignment in SEQ ID NO 2613: from 1 to 19
- Alignment No. 16165
- gi No. 4995696
- % Identity 95.5
- Alignment Length 22
- Location of Alignment in SEQ ID NO 2613: from 1 to 19
- Alignment No. 16166
- gi No. 4995737
- % Identity 82.6
- Alignment Length 23
- Location of Alignment in SEQ ID NO 2613: from 1 to 20
- Alignment No. 16167
- gi No. 4995739
- % Identity 91.3
- Alignment Length 23
- Location of Alignment in SEQ ID NO 2613: from 1 to 20
- Alignment No. 16168
- gi No. 508526
- % Identity 90.8
- Alignment Length 131
- Location of Alignment in SEQ ID NO 2613: from 1 to 80
- Alignment No. 16169
- gi No. 535428
- % Identity 76
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2613: from 1 to 94
- Alignment No. 16170
- gi No. 552252
- % Identity 84.6
- Alignment Length 26
- Location of Alignment in SEQ ID NO 2613: from 24 to 49
- Alignment No. 16171
- gi No. 5640002
- % Identity 91.3
- Alignment Length 80
- Location of Alignment in SEQ ID NO 2613: from 10 to 89

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- Alignment No. 16172
- gi No. 565166
- % Identity 86.2
- Alignment Length 145
- Location of Alignment in SEQ ID NO 2613: from 1 to 94
- Alignment No. 16173
- gi No. 576081
- % Identity 89.4
- Alignment Length 141
- Location of Alignment in SEQ ID NO 2613: from 1 to 94
- Alignment No. 16174
- gi No. 587454
- % Identity 90.5
- Alignment Length 137
- Location of Alignment in SEQ ID NO 2613: from 1 to 94
- Alignment No. 16175
- gi No. 640285
- % Identity 91
- Alignment Length 145
- Location of Alignment in SEQ ID NO 2613: from 1 to 94
- Alignment No. 16176
- gi No. 640294
- % Identity 90.8
- Alignment Length 142
- Location of Alignment in SEQ ID NO 2613: from 1 to 94
- Alignment No. 16177
- gi No. 71660
- % Identity 90.3
- Alignment Length 145
- Location of Alignment in SEQ ID NO 2613: from 1 to 94 $\,$
- Alignment No. 16178
- gi No. 71662
- % Identity 91
- Alignment Length 145
- Location of Alignment in SEQ ID NO 2613: from 1 to 94 $\,$
- Alignment No. 16179
- gi No. 71667
- % Identity 91.7
- Alignment Length 145
- Location of Alignment in SEQ ID NO 2613: from 1 to 94
- Alignment No. 16180
- gi No. 71673
- % Identity 90.3
- Alignment Length 145
- Location of Alignment in SEQ ID NO 2613: from 1 to 94
- Alignment No. 16181
- gi No. 71676
- % Identity 84.8
- Alignment Length 145
- Location of Alignment in SEQ ID NO 2613: from 1 to 94
- Alignment No. 16182

- qi No. 729010
- % Identity 98.6
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2613: from 1 to 94
- Alignment No. 16183
- gi No. 729011
- % Identity 82.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2613: from 1 to 94
- Alignment No. 16184
- gi No. 729012
- % Identity 87.3
- Alignment Length 142
- Location of Alignment in SEQ ID NO 2613: from 1 to 94
- Alignment No. 16185
- gi No. 809298
- % Identity 86.9
- Alignment Length 145
- Location of Alignment in SEQ ID NO 2613: from 1 to 94
- Alignment No. 16186
- gi No. 85332
- % Identity 92.2
- Alignment Length 141
- Location of Alignment in SEQ ID NO 2613: from 1 to 91
- Alignment No. 16187
- gi No. 9874
- % Identity 85.6
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2613: from 1 to 94
- Alignment No. 16188
- gi No. 99673
- % Identity 81.9
- Alignment Length 72
- Location of Alignment in SEQ ID NO 2613: from 1 to 23

Maximum Length Sequence corresponding to clone ID 316301

- (A) Polynucleotide Sequence
 - Pat. Appln. SEQ ID NO 2614
 - Ceres seq id 1504001
 - (B) Polypeptide Sequence
 - Pat. Appln. SEQ ID NO 2615
 - Ceres seq id 1504002
 - Location of start within SEQ ID NO 2614: at 1 nt.
- - (D) Related Amino Acid Sequences
 - (B) Polypeptide Sequence
 - Pat. Appln. SEQ ID NO 2616
 - Ceres seq_id 1504003
 - Location of start within SEQ ID NO 2614: at 2 nt.

- Alignment No. 16189
- Ribosomal protein L5
- Location within SEQ ID NO 2616: from 34 to 79 aa.
- (D) Related Amino Acid Sequences
 - Alignment No. 16190
 - gi No. 1125808
 - % Identity 80.4
 - Alignment Length 51
 - Location of Alignment in SEQ ID NO 2616: from 29 to 79
 - Alignment No. 16191
 - gi No. 1172816
 - % Identity 90.7
 - Alignment Length 54
 - Location of Alignment in SEQ ID NO 2616: from 26 to 79
 - Alignment No. 16192
 - gi No. 1172817
 - % Identity 90.6
 - Alignment Length 53
 - Location of Alignment in SEQ ID NO 2616: from 27 to 79
 - Alignment No. 16193
 - gi No. 1172952
 - % Identity 71.1
 - Alignment Length 45
 - Location of Alignment in SEQ ID NO 2616: from 35 to 79
 - Alignment No. 16194
 - qi No. 1172954
 - % Identity 70.6
 - Alignment Length 51
 - Location of Alignment in SEQ ID NO 2616: from 26 to 76
 - Alignment No. 16195
 - gi No. 1172969
 - % Identity 90.7
 - Alignment Length 54
 - Location of Alignment in SEQ ID NO 2616: from 26 to 79
 - Alignment No. 16196
 - gi No. 1173055
 - % Identity 94.4
 - Alignment Length 54
 - Location of Alignment in SEQ ID NO 2616: from 26 to 79
 - Alignment No. 16197
 - gi No. 132649
 - % Identity 70.9
 - Alignment Length 55
 - Location of Alignment in SEQ ID NO 2616: from 26 to 79
 - Alignment No. 16198
 - gi No. 132951
 - % Identity 79.6
 - Alignment Length 49
 - Location of Alignment in SEQ ID NO 2616: from 31 to 79
 - Alignment No. 16199
 - gi No. 132992

- % Identity 75
- Alignment Length 44
- Location of Alignment in SEQ ID NO 2616: from 36 to 79
- Alignment No. 16200
- gi No. 1350658
- % Identity 70.9
- Alignment Length 55
- Location of Alignment in SEQ ID NO 2616: from 26 to 79
- Alignment No. 16201
- gi No. 1350659
- % Identity 70.6
- Alignment Length 51
- Location of Alignment in SEQ ID NO 2616: from 26 to 76
- Alignment No. 16202
- qi No. 1710494
- % Identity 78
- Alignment Length 50
- Location of Alignment in SEQ ID NO 2616: from 30 to 79
- Alignment No. 16203
- gi No. 2500240
- % Identity 80.4
- Alignment Length 51
- Location of Alignment in SEQ ID NO 2616: from 29 to 79
- Alignment No. 16204
- gi No. 2500241
- % Identity 78.4
- Alignment Length 51
- Location of Alignment in SEQ ID NO 2616: from 29 to 79
- Alignment No. 16205
- gi No. 2570507
- % Identity 85.2
- Alignment Length 54
- Location of Alignment in SEQ ID NO 2616: from 26 to 79
- Alignment No. 16206
- gi No. 4322
- % Identity 77.6
- Alignment Length 49
- Location of Alignment in SEQ ID NO 2616: from 31 to 79
- Alignment No. 16207
- gi No. 4432750
- % Identity 86.1
- Alignment Length 36
- Location of Alignment in SEQ ID NO 2616: from 41 to 76
- Alignment No. 16208
- gi No. 4512679
- % Identity 74.1
- Alignment Length 54
- Location of Alignment in SEQ ID NO 2616: from 36 to 79
- Alignment No. 16209
- gi No. 4586222
- % Identity 76.5

- Alignment Length 51
- Location of Alignment in SEQ ID NO 2616: from 29 to 79
- Alignment No. 16210
- gi No. 71107
- % Identity 79.6
- Alignment Length 49
- Location of Alignment in SEQ ID NO 2616: from 31 to 79
- (B) Polypeptide Sequence
 - Pat. Appln. SEQ ID NO 2617
 - Ceres seq id 1504004
 - Location of start within SEQ ID NO 2614: at 3 nt.
- (C) Nomination and Annotation of Domains within Predicted Polypeptide(s) $% \left(\frac{1}{2}\right) =\frac{1}{2}\left(\frac{1}{2}\right) +\frac{1}{2}\left(\frac{1}{2}\right) +\frac{$
 - (D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 316327

- (A) Polynucleotide Sequence
 - Pat. Appln. SEQ ID NO 2618
 - Ceres seq_id 1504016
 - (B) Polypeptide Sequence
 - Pat. Appln. SEQ ID NO 2619
 - Ceres seq_id 1504017
 - Location of start within SEQ ID NO 2618: at 3 nt.
- (C) Nomination and Annotation of Domains within Predicted Polypeptide(s)
 - (D) Related Amino Acid Sequences
 - (B) Polypeptide Sequence
 - Pat. Appln. SEQ ID NO 2620
 - Ceres seq id 1504018
 - Location of start within SEQ ID NO 2618: at 310 nt.
- (C) Nomination and Annotation of Domains within Predicted Polypeptide(s) $% \left(\frac{1}{2}\right) =\frac{1}{2}\left(\frac{1}{2}\right) +\frac{1}{2}\left(\frac{1}{2}\right) +\frac{$
 - (D) Related Amino Acid Sequences
 - Alignment No. 16211
 - gi No. 2224915
 - % Identity 81.8
 - Alignment Length 77
 - Location of Alignment in SEQ ID NO 2620: from 1 to 55
 - Alignment No. 16212
 - gi No. 729944
 - % Identity 75
 - Alignment Length 56
 - Location of Alignment in SEQ ID NO 2620: from 1 to $55\,$

Maximum Length Sequence corresponding to clone ID 316354

- (A) Polynucleotide Sequence
 - Pat. Appln. SEQ ID NO 2621
 - Ceres seq_id 1504025
 - (B) Polypeptide Sequence
 - Pat. Appln. SEQ ID NO 2622
 - Ceres seq_id 1504026
 - Location of start within SEQ ID NO 2621: at 133 nt.

- (C) Nomination and Annotation of Domains within Predicted Polypeptide(s)
 - Alignment No. 16213
 - Sugar (and other) transporter
 - Location within SEQ ID NO 2622: from 1 to 98 aa.
 - (D) Related Amino Acid Sequences
 - Alignment No. 16214
 - gi No. 2760325
 - % Identity 73.1
 - Alignment Length 108
 - Location of Alignment in SEQ ID NO 2622: from 1 to 98
 - (B) Polypeptide Sequence
 - Pat. Appln. SEQ ID NO 2623
 - Ceres seq_id 1504027
 - Location of start within SEQ ID NO 2621: at 166 nt.
- - Alignment No. 16215
 - Sugar (and other) transporter
 - Location within SEQ ID NO 2623: from 1 to 87 aa.
 - (D) Related Amino Acid Sequences
 - Alignment No. 16216
 - gi No. 2760325
 - % Identity 73.1
 - Alignment Length 108
 - Location of Alignment in SEQ ID NO 2623: from 1 to 87

- (A) Polynucleotide Sequence
 - Pat. Appln. SEQ ID NO 2624
 - Ceres seq_id 1504036
 - (B) Polypeptide Sequence
 - Pat. Appln. SEQ ID NO 2625
 - Ceres seq_id 1504037
 - Location of start within SEQ ID NO 2624: at 3 nt.
- (C) Nomination and Annotation of Domains within Predicted Polypeptide(s)
 - (D) Related Amino Acid Sequences
 - Alignment No. 16217
 - gi No. 2505870
 - % Identity 78.3
 - Alignment Length 152
 - Location of Alignment in SEQ ID NO 2625: from 1 to 152
 - Alignment No. 16218
 - gi No. 3287679
 - % Identity 80.4
 - Alignment Length 138
 - Location of Alignment in SEQ ID NO 2625: from 1 to 138 $\,$
 - (B) Polypeptide Sequence
 - Pat. Appln. SEQ ID NO 2626
 - Ceres seq id 1504038
 - Location of start within SEQ ID NO 2624: at 75 nt.

- - (D) Related Amino Acid Sequences
 - Alignment No. 16219
 - gi No. 2505870
 - % Identity 78.3
 - Alignment Length 152
 - Location of Alignment in SEQ ID NO 2626: from 1 to 128
 - Alignment No. 16220
 - gi No. 3287679
 - % Identity 80.4
 - Alignment Length 138
 - Location of Alignment in SEQ ID NO 2626: from 1 to 114
 - (B) Polypeptide Sequence
 - Pat. Appln. SEQ ID NO 2627
 - Ceres seq id 1504039
 - Location of start within SEQ ID NO 2624: at 81 nt.
- - (D) Related Amino Acid Sequences
 - Alignment No. 16221
 - gi No. 2505870
 - % Identity 78.3
 - Alignment Length 152
 - Location of Alignment in SEQ ID NO 2627: from 1 to 126
 - Alignment No. 16222
 - gi No. 3287679
 - % Identity 80.4
 - Alignment Length 138
 - Location of Alignment in SEQ ID NO 2627: from 1 to 112

- (A) Polynucleotide Sequence
 - Pat. Appln. SEQ ID NO 2628
 - Ceres seq_id 1504044
 - (B) Polypeptide Sequence
 - Pat. Appln. SEQ ID NO 2629
 - Ceres seq_id 1504045
 - Location of start within SEQ ID NO 2628: at 1 nt.
- (C) Nomination and Annotation of Domains within Predicted Polypeptide(s) $\label{eq:condition} % \begin{array}{c} \text{Polyperiod} \\ \text{Poly$
 - (D) Related Amino Acid Sequences
 - Alignment No. 16223
 - gi No. 3057044
 - % Identity 70.7
 - Alignment Length 82
 - Location of Alignment in SEQ ID NO 2629: from 61 to 142
 - Alignment No. 16224
 - gi No. 3337356
 - % Identity 93.9
 - Alignment Length 82
 - Location of Alignment in SEQ ID NO 2629: from 61 to 142
 - Alignment No. 16225
 - gi No. 3834321

- % Identity 92.7
- Alignment Length 82
- Location of Alignment in SEQ ID NO 2629: from 61 to 142
- Alignment No. 16226
- gi No. 3881191
- % Identity 70.5
- Alignment Length 78
- Location of Alignment in SEQ ID NO 2629: from 65 to 142
- Alignment No. 16227
- gi No. 4689112
- % Identity 70.7
- Alignment Length 82
- Location of Alignment in SEQ ID NO 2629: from 61 to 142
- Alignment No. 16228
- gi No. 585957
- % Identity 70.7
- Alignment Length 82
- Location of Alignment in SEQ ID NO 2629: from 61 to 142
- Alignment No. 16229
- gi No. 585959
- % Identity 70.7
- Alignment Length 82
- Location of Alignment in SEQ ID NO 2629: from 61 to 142

- (A) Polynucleotide Sequence
 - Pat. Appln. SEQ ID NO 2630
 - Ceres seq_id 1504050
 - (B) Polypeptide Sequence
 - Pat. Appln. SEQ ID NO 2631
 - Ceres seq_id 1504051
 - Location of start within SEQ ID NO 2630: at 2 nt.
- (C) Nomination and Annotation of Domains within Predicted Polypeptide(s) $% \left(\frac{1}{2}\right) =\frac{1}{2}\left(\frac{1}{2}\right) +\frac{1}{2}\left(\frac{1}{2}\right) +\frac{$
 - Alignment No. 16230
 - WD domain, G-beta repeat
 - Location within SEQ ID NO 2631: from 85 to 124 aa.
 - (D) Related Amino Acid Sequences
 - Alignment No. 16231
 - gi No. 3122386
 - % Identity 83.2
 - Alignment Length 167
 - Location of Alignment in SEQ ID NO 2631: from 1 to 166 $\,$
 - Alignment No. 16232
 - gi No. 3122387
 - % Identity 86.8
 - Alignment Length 167
 - Location of Alignment in SEQ ID NO 2631: from 1 to 166

- (A) Polynucleotide Sequence
 - Pat. Appln. SEQ ID NO 2632
 - Ceres seq id 1504098
 - (B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2633
- Ceres seq id 1504099
- Location of start within SEQ ID NO 2632: at 125 nt.
- (C) Nomination and Annotation of Domains within Predicted Polypeptide(s)
 - Alignment No. 16233
 - ADP-ribosylation factor family
 - Location within SEQ ID NO 2633: from 2 to 75 aa.
 - Alignment No. 16234
 - Ras family
 - Location within SEQ ID NO 2633: from 19 to 80 aa.
 - (D) Related Amino Acid Sequences
 - Alignment No. 16235
 - gi No. 114122
 - % Identity 70.7
 - Alignment Length 75
 - Location of Alignment in SEQ ID NO 2633: from 1 to 75
 - Alignment No. 16236
 - gi No. 3252999
 - % Identity 74.1
 - Alignment Length 58
 - Location of Alignment in SEQ ID NO 2633: from 18 to 75
 - Alignment No. 16237
 - gi No. 3746799
 - % Identity 71.9
 - Alignment Length 57
 - Location of Alignment in SEQ ID NO 2633: from 19 to 75
 - Alignment No. 16238
 - gi No. 3746801
 - % Identity 71.9
 - Alignment Length 57
 - Location of Alignment in SEQ ID NO 2633: from 19 to 75
 - Alignment No. 16239
 - gi No. 461532
 - % Identity 70.7
 - Alignment Length 75
 - Location of Alignment in SEQ ID NO 2633: from 1 to 75
 - Alignment No. 16240
 - gi No. 89370
 - % Identity 76.2
 - Alignment Length 21
 - Location of Alignment in SEQ ID NO 2633: from 22 to 42
 - (B) Polypeptide Sequence
 - Pat. Appln. SEQ ID NO 2634
 - Ceres seq_id 1504100
 - Location of start within SEQ ID NO 2632: at 176 nt.
- (C) Nomination and Annotation of Domains within Predicted Polypeptide(s)
 - Alignment No. 16241
 - ADP-ribosylation factor family
 - Location within SEQ ID NO 2634: from 1 to 58 aa.

- Alignment No. 16242
- Ras family
- Location within SEQ ID NO 2634: from 2 to 63 aa.
- (D) Related Amino Acid Sequences
 - Alignment No. 16243
 - gi No. 114122
 - % Identity 70.7
 - Alignment Length 75
 - Location of Alignment in SEQ ID NO 2634: from 1 to 58
 - Alignment No. 16244
 - gi No. 3252999
 - % Identity 74.1
 - Alignment Length 58
 - Location of Alignment in SEQ ID NO 2634: from 1 to 58
 - Alignment No. 16245
 - gi No. 3746799
 - % Identity 71.9
 - Alignment Length 57
 - Location of Alignment in SEQ ID NO 2634: from 2 to 58
 - Alignment No. 16246
 - gi No. 3746801
 - % Identity 71.9
 - Alignment Length 57
 - Location of Alignment in SEQ ID NO 2634: from 2 to 58
 - Alignment No. 16247
 - gi No. 461532
 - % Identity 70.7
 - Alignment Length 75
 - Location of Alignment in SEQ ID NO 2634: from 1 to 58
 - Alignment No. 16248
 - gi No. 89370
 - % Identity 76.2
 - Alignment Length 21
 - Location of Alignment in SEQ ID NO 2634: from 5 to 25
- (B) Polypeptide Sequence
 - Pat. Appln. SEQ ID NO 2635
 - Ceres seq_id 1504101
 - Location of start within SEQ ID NO 2632: at 188 nt.
- - Alignment No. 16249
 - ADP-ribosylation factor family
 - Location within SEQ ID NO 2635: from 1 to 54 aa.
 - Alignment No. 16250
 - Ras family
 - Location within SEQ ID NO 2635: from 1 to 59 aa.
 - (D) Related Amino Acid Sequences
 - Alignment No. 16251
 - gi No. 114122
 - % Identity 70.7

- Alignment Length 75
- Location of Alignment in SEQ ID NO 2635: from 1 to 54
- Alignment No. 16252
- gi No. 3252999
- % Identity 74.1
- Alignment Length 58
- Location of Alignment in SEQ ID NO 2635: from 1 to 54
- Alignment No. 16253
- gi No. 3746799
- % Identity 71.9
- Alignment Length 57
- Location of Alignment in SEQ ID NO 2635: from 1 to 54
- Alignment No. 16254
- gi No. 3746801
- % Identity 71.9
- Alignment Length 57
- Location of Alignment in SEQ ID NO 2635: from 1 to 54
- Alignment No. 16255
- gi No. 461532
- % Identity 70.7
- Alignment Length 75
- Location of Alignment in SEQ ID NO 2635: from 1 to 54
- Alignment No. 16256
- gi No. 89370
- % Identity 76.2
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2635: from 1 to 21

- (A) Polynucleotide Sequence
 - Pat. Appln. SEQ ID NO 2636
 - Ceres seq_id 1504102
 - (B) Polypeptide Sequence
 - Pat. Appln. SEQ ID NO 2637
 - Ceres seq_id 1504103
 - Location of start within SEQ ID NO 2636: at 2 nt.
- - (D) Related Amino Acid Sequences
 - Alignment No. 16257
 - gi No. 462338
 - % Identity 71.4
 - Alignment Length 14
 - Location of Alignment in SEQ ID NO 2637: from 95 to 108
 - (B) Polypeptide Sequence
 - Pat. Appln. SEQ ID NO 2638
 - Ceres seq_id 1504104
 - Location of start within SEQ ID NO 2636: at 3 nt.
- - (D) Related Amino Acid Sequences
 - (B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2639
- Ceres seq_id 1504105
- Location of start within SEQ ID NO 2636: at 94 nt.
- - Alignment No. 16258
 - Merozoite Surface Antigen 2 (MSA-2) family
 - Location within SEQ ID NO 2639: from 20 to 98 aa.
 - (D) Related Amino Acid Sequences

- (A) Polynucleotide Sequence
 - Pat. Appln. SEQ ID NO 2640
 - Ceres seq_id 1504107
 - (B) Polypeptide Sequence
 - Pat. Appln. SEQ ID NO 2641
 - Ceres seq_id 1504108
 - Location of start within SEQ ID NO 2640: at 2 nt.
- (C) Nomination and Annotation of Domains within Predicted Polypeptide(s) $% \left(1\right) =\left(1\right) \left(1\right) +\left(1\right) \left(1\right) \left(1\right) +\left(1\right) \left(1\right)$
 - Alignment No. 16259
 - Eukaryotic ribosomal protein L18
 - Location within SEQ ID NO 2641: from 65 to 155 aa.
 - (D) Related Amino Acid Sequences
 - Alignment No. 16260
 - gi No. 1172977
 - % Identity 78.4
 - Alignment Length 102
 - Location of Alignment in SEQ ID NO 2641: from 55 to 155
 - Alignment No. 16261
 - gi No. 2529670
 - % Identity 74.3
 - Alignment Length 101
 - Location of Alignment in SEQ ID NO 2641: from 56 to 155
 - Alignment No. 16262
 - gi No. 3021348
 - % Identity 75.8
 - Alignment Length 99
 - Location of Alignment in SEQ ID NO 2641: from 58 to 155
 - (B) Polypeptide Sequence
 - Pat. Appln. SEQ ID NO 2642
 - Ceres seq id 1504109
 - Location of start within SEQ ID NO 2640: at 3 nt.
- (C) Nomination and Annotation of Domains within Predicted Polypeptide(s) $\label{eq:condition} % \begin{array}{c} \text{Polyperiod} \\ \text{Poly$
 - (D) Related Amino Acid Sequences
 - (B) Polypeptide Sequence
 - Pat. Appln. SEQ ID NO 2643
 - Ceres seq_id 1504110
 - Location of start within SEQ ID NO 2640: at 164 nt.

- (C) Nomination and Annotation of Domains within Predicted Polypeptide(s)
 - Alignment No. 16263
 - Eukaryotic ribosomal protein L18
 - Location within SEQ ID NO 2643: from 11 to 101 aa.
 - (D) Related Amino Acid Sequences
 - Alignment No. 16264
 - gi No. 1172977
 - % Identity 78.4
 - Alignment Length 102
 - Location of Alignment in SEQ ID NO 2643: from 1 to 101
 - Alignment No. 16265
 - gi No. 2529670
 - % Identity 74.3
 - Alignment Length 101
 - Location of Alignment in SEQ ID NO 2643: from 2 to 101
 - Alignment No. 16266
 - gi No. 3021348
 - % Identity 75.8
 - Alignment Length 99
 - Location of Alignment in SEQ ID NO 2643: from 4 to 101

- (A) Polynucleotide Sequence
 - Pat. Appln. SEQ ID NO 2644
 - Ceres seq_id 1504111
 - (B) Polypeptide Sequence
 - Pat. Appln. SEQ ID NO 2645
 - Ceres seq id 1504112
 - Location of start within SEQ ID NO 2644: at 1 nt.
- (C) Nomination and Annotation of Domains within Predicted Polypeptide(s) $% \left(\frac{1}{2}\right) =\frac{1}{2}\left(\frac{1}{2}\right) +\frac{1}{2}\left(\frac{1}{2}\right) +\frac{$
 - (D) Related Amino Acid Sequences
 - Alignment No. 16267
 - gi No. 121928
 - % Identity 75
 - Alignment Length 12
 - Location of Alignment in SEQ ID NO 2645: from 30 to 40
 - Alignment No. 16268
 - gi No. 121950
 - % Identity 92.3
 - Alignment Length 26
 - Location of Alignment in SEQ ID NO 2645: from 17 to 42
 - (B) Polypeptide Sequence
 - Pat. Appln. SEQ ID NO 2646
 - Ceres seq_id 1504113
 - Location of start within SEQ ID NO 2644: at 49 nt.
- - (D) Related Amino Acid Sequences
 - Alignment No. 16269
 - gi No. 121928
 - % Identity 75
 - Alignment Length 12

- Location of Alignment in SEQ ID NO 2646: from 14 to 24
- Alignment No. 16270
- gi No. 121950
- % Identity 92.3
- Alignment Length 26
- Location of Alignment in SEQ ID NO 2646: from 1 to 26
- (B) Polypeptide Sequence
 - Pat. Appln. SEQ ID NO 2647
 - Ceres seq_id 1504114
 - Location of start within SEQ ID NO 2644: at 212 nt.
- - Alignment No. 16271
 - linker histone H1 and H5 family
 - Location within SEQ ID NO 2647: from 1 to 65 aa.
 - (D) Related Amino Acid Sequences
 - Alignment No. 16272
 - gi No. 121906
 - % Identity 81.8
 - Alignment Length 22
 - Location of Alignment in SEQ ID NO 2647: from 1 to 22
 - Alignment No. 16273
 - gi No. 121950
 - % Identity 87.6
 - Alignment Length 97
 - Location of Alignment in SEQ ID NO 2647: from 1 to 73
 - Alignment No. 16274
 - gi No. 121958
 - % Identity 70.5
 - Alignment Length 95
 - Location of Alignment in SEQ ID NO 2647: from 1 to 69
 - Alignment No. 16275
 - gi No. 5230781
 - % Identity 70.5
 - Alignment Length 95
 - Location of Alignment in SEQ ID NO 2647: from 1 to 69
 - Alignment No. 16276
 - gi No. 5230783
 - % Identity 70.5
 - Alignment Length 95
 - Location of Alignment in SEQ ID NO 2647: from 1 to 69
 - Alignment No. 16277
 - gi No. 5230785
 - % Identity 76.3
 - Alignment Length 93
 - Location of Alignment in SEQ ID NO 2647: from 1 to 69
 - Alignment No. 16278
 - gi No. 5230788
 - % Identity 71.6
 - Alignment Length 95
 - Location of Alignment in SEQ ID NO 2647: from 1 to 69

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- Alignment No. 16279
- gi No. 5230790
- % Identity 70.5
- Alignment Length 95
- Location of Alignment in SEQ ID NO 2647: from 1 to 69

- (A) Polynucleotide Sequence
 - Pat. Appln. SEQ ID NO 2648
 - Ceres seq_id 1504119
 - (B) Polypeptide Sequence
 - Pat. Appln. SEQ ID NO 2649
 - Ceres seq_id 1504120
 - Location of start within SEQ ID NO 2648: at 1 nt.
- (C) Nomination and Annotation of Domains within Predicted Polypeptide(s) $% \left(\frac{1}{2}\right) =\frac{1}{2}\left(\frac{1}{2}\right) +\frac{1}{2}\left(\frac{1}{2}\right) +\frac{$
 - (D) Related Amino Acid Sequences
 - Alignment No. 16280
 - gi No. 1085819
 - % Identity 72.7
 - Alignment Length 11
 - Location of Alignment in SEQ ID NO 2649: from 74 to 84
 - (B) Polypeptide Sequence
 - Pat. Appln. SEQ ID NO 2650
 - Ceres seq_id 1504121
 - Location of start within SEQ ID NO 2648: at 3 nt.
- (C) Nomination and Annotation of Domains within Predicted Polypeptide(s) $% \left(\frac{1}{2}\right) =\frac{1}{2}\left(\frac{1}{2}\right) +\frac{1}{2}\left(\frac{1}{2}\right) +\frac{$
 - (D) Related Amino Acid Sequences
 - Alignment No. 16281
 - gi No. 137715
 - % Identity 71.4
 - Alignment Length 15
 - Location of Alignment in SEQ ID NO 2650: from 24 to 37
 - Alignment No. 16282
 - gi No. 1389772
 - % Identity 76.9
 - Alignment Length 13
 - Location of Alignment in SEQ ID NO 2650: from 57 to 69
 - Alignment No. 16283
 - gi No. 1914851
 - % Identity 78.6
 - Alignment Length 14
 - Location of Alignment in SEQ ID NO 2650: from 57 to 70
 - Alignment No. 16284
 - gi No. 2388805
 - % Identity 76.9
 - Alignment Length 13
 - Location of Alignment in SEQ ID NO 2650: from 57 to 69
 - Alignment No. 16285
 - gi No. 3183204
 - % Identity 76.9
 - Alignment Length 13

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- Location of Alignment in SEQ ID NO 2650: from 57 to 69 - Alignment No. 16286 - gi No. 322755 - % Identity 71.4 - Alignment Length 14 - Location of Alignment in SEQ ID NO 2650: from 25 to 38 - Alignment No. 16287 - gi No. 333063 - % Identity 71.4 - Alignment Length 15 - Location of Alignment in SEQ ID NO 2650: from 24 to 37 - Alignment No. 16288 - gi No. 465445 - % Identity 76.9 - Alignment Length 13 - Location of Alignment in SEQ ID NO 2650: from 57 to 69 - Alignment No. 16289 - gi No. 539029 - % Identity 71.4 - Alignment Length 14
- Location of Alignment in SEQ ID NO 2650: from 25 to 38
- Alignment No. 16290
- gi No. 553165
- % Identity 75
- Alignment Length 12
- Location of Alignment in SEQ ID NO 2650: from 58 to 69
- Alignment No. 16291
- gi No. 553165
- % Identity 76.9
- Alignment Length 13
- Location of Alignment in SEQ ID NO 2650: from 57 to 69
- Alignment No. 16292
- gi No. 624076
- % Identity 72.7
- Alignment Length 11
- Location of Alignment in SEQ ID NO 2650: from 59 to 69
- Alignment No. 16293
- gi No. 729462
- % Identity 76.9
- Alignment Length 13
- Location of Alignment in SEQ ID NO 2650: from 57 to 69
- Alignment No. 16294
- gi No. 93144
- % Identity 76.9
- Alignment Length 13
- Location of Alignment in SEQ ID NO 2650: from 57 to 69
- (B) Polypeptide Sequence
 - Pat. Appln. SEQ ID NO 2651
 - Ceres seq id 1504122
 - Location of start within SEQ ID NO 2648: at 90 nt.

- (C) Nomination and Annotation of Domains within Predicted Polypeptide(s)
 - (D) Related Amino Acid Sequences
 - Alignment No. 16295
 - gi No. 1389772
 - % Identity 76.9
 - Alignment Length 13
 - Location of Alignment in SEQ ID NO 2651: from 28 to 40
 - Alignment No. 16296
 - gi No. 1914851
 - % Identity 78.6
 - Alignment Length 14
 - Location of Alignment in SEQ ID NO 2651: from 28 to 41
 - Alignment No. 16297
 - qi No. 2388805
 - % Identity 76.9
 - Alignment Length 13
 - Location of Alignment in SEQ ID NO 2651: from 28 to 40
 - Alignment No. 16298
 - gi No. 3183204
 - % Identity 76.9
 - Alignment Length 13
 - Location of Alignment in SEQ ID NO 2651: from 28 to 40
 - Alignment No. 16299
 - gi No. 465445
 - % Identity 76.9
 - Alignment Length 13
 - Location of Alignment in SEQ ID NO 2651: from 28 to 40
 - Alignment No. 16300
 - gi No. 553165
 - % Identity 75
 - Alignment Length 12
 - Location of Alignment in SEQ ID NO 2651: from 29 to 40
 - Alignment No. 16301
 - gi No. 553165
 - % Identity 76.9
 - Alignment Length 13
 - Location of Alignment in SEQ ID NO 2651: from 28 to 40
 - Alignment No. 16302
 - gi No. 624076
 - % Identity 72.7
 - Alignment Length 11
 - Location of Alignment in SEQ ID NO 2651: from 30 to 40
 - Alignment No. 16303
 - gi No. 729462
 - % Identity 76.9
 - Alignment Length 13
 - Location of Alignment in SEQ ID NO 2651: from 28 to 40
 - Alignment No. 16304
 - gi No. 93144
 - % Identity 76.9
 - Alignment Length 13

- Location of Alignment in SEQ ID NO 2651: from 28 to 40

Maximum Length Sequence corresponding to clone ID 316862

- (A) Polynucleotide Sequence
 - Pat. Appln. SEQ ID NO 2652
 - Ceres seq id 1504161
 - (B) Polypeptide Sequence
 - Pat. Appln. SEQ ID NO 2653
 - Ceres seq id 1504162
 - Location of start within SEQ ID NO 2652: at 3 nt.
- (C) Nomination and Annotation of Domains within Predicted Polypeptide(s)
 - (D) Related Amino Acid Sequences
 - Alignment No. 16305
 - gi No. 1916974
 - % Identity 75
 - Alignment Length 16
 - Location of Alignment in SEQ ID NO 2653: from 7 to 21
 - Alignment No. 16306
 - gi No. 477833
 - % Identity 75
 - Alignment Length 16
 - Location of Alignment in SEQ ID NO 2653: from 7 to 21

- (A) Polynucleotide Sequence
 - Pat. Appln. SEQ ID NO 2654
 - Ceres seq_id 1504170
 - (B) Polypeptide Sequence
 - Pat. Appln. SEQ ID NO 2655
 - Ceres seq id 1504171
 - Location of start within SEQ ID NO 2654: at 1 nt.
- (C) Nomination and Annotation of Domains within Predicted Polypeptide(s) $\label{eq:continuous}$
 - (D) Related Amino Acid Sequences
 - Alignment No. 16307
 - gi No. 404077
 - % Identity 70.6
 - Alignment Length 17
 - Location of Alignment in SEQ ID NO 2655: from 30 to 46
 - (B) Polypeptide Sequence
 - Pat. Appln. SEQ ID NO 2656
 - Ceres seq_id 1504172
 - Location of start within SEQ ID NO 2654: at 2 nt.
- (C) Nomination and Annotation of Domains within Predicted Polypeptide(s) $\label{eq:condition}$
 - (D) Related Amino Acid Sequences
 - Alignment No. 16308
 - gi No. 4972116
 - % Identity 81.8
 - Alignment Length 11
 - Location of Alignment in SEQ ID NO 2656: from 26 to 36
 - (B) Polypeptide Sequence
 - Pat. Appln. SEQ ID NO 2657
 - Ceres seq_id 1504173

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- Location of start within SEQ ID NO 2654: at 3 nt.
- - (D) Related Amino Acid Sequences
 - Alignment No. 16309
 - gi No. 4996642
 - % Identity 72.7
 - Alignment Length 11
 - Location of Alignment in SEQ ID NO 2657: from 17 to 27

- (A) Polynucleotide Sequence
 - Pat. Appln. SEQ ID NO 2658
 - Ceres seq_id 1504178
 - (B) Polypeptide Sequence
 - Pat. Appln. SEQ ID NO 2659
 - Ceres seq id 1504179
 - Location of start within SEQ ID NO 2658: at 3 nt.
- - Alignment No. 16310
 - GDP dissociation inhibitor
 - Location within SEQ ID NO 2659: from 1 to 60 aa.
 - (D) Related Amino Acid Sequences
 - Alignment No. 16311
 - gi No. 1550740
 - % Identity 73.8
 - Alignment Length 61Location of Alignment in SEQ ID NO 2659: from 1 to 60
 - Alignment No. 16312
 - gi No. 1655424
 - % Identity 73.8
 - Alignment Length 61
 - Location of Alignment in SEQ ID NO 2659: from 1 to 60
 - Alignment No. 16313
 - qi No. 2384758
 - % Identity 88.5
 - Alignment Length 61
 - Location of Alignment in SEQ ID NO 2659: from 1 to 60
 - Alignment No. 16314
 - gi No. 2384760
 - % Identity 85.2
 - Alignment Length 61
 - Location of Alignment in SEQ ID NO 2659: from 1 to 60
 - Alignment No. 16315
 - gi No. 2446981
 - % Identity 73.8
 - Alignment Length 61
 - Location of Alignment in SEQ ID NO 2659: from 1 to 60
 - Alignment No. 16316
 - gi No. 2501850
 - % Identity 90.2
 - Alignment Length 61

- Location of Alignment in SEQ ID NO 2659: from 1 to 60
- Alignment No. 16317
- gi No. 3175990
- % Identity 88.5
- Alignment Length 61
- Location of Alignment in SEQ ID NO 2659: from 1 to 60

- (A) Polynucleotide Sequence
 - Pat. Appln. SEQ ID NO 2660
 - Ceres seq_id 1504180
 - (B) Polypeptide Sequence
 - Pat. Appln. SEQ ID NO 2661
 - Ceres seq_id 1504181
 - Location of start within SEQ ID NO 2660: at 1 nt.
- - (D) Related Amino Acid Sequences
 - (B) Polypeptide Sequence
 - Pat. Appln. SEQ ID NO 2662
 - Ceres seq_id 1504182
 - Location of start within SEQ ID NO 2660: at 2 nt.
- - Alignment No. 16318
 - Globin
 - Location within SEQ ID NO 2662: from 44 to 168 aa.
 - (D) Related Amino Acid Sequences
 - (B) Polypeptide Sequence
 - Pat. Appln. SEQ ID NO 2663
 - Ceres seq_id 1504183
 - Location of start within SEQ ID NO 2660: at 101 nt.
- (C) Nomination and Annotation of Domains within Predicted Polypeptide(s)
 - Alignment No. 16319
 - Globin
 - Location within SEQ ID NO 2663: from 11 to 135 aa.
 - (D) Related Amino Acid Sequences

- (A) Polynucleotide Sequence
 - Pat. Appln. SEQ ID NO 2664
 - Ceres seq_id 1504184
 - (B) Polypeptide Sequence
 - Pat. Appln. SEQ ID NO 2665
 - Ceres seq_id 1504185
 - Location of start within SEQ ID NO 2664: at 3 nt.
- - Alignment No. 16320
 - Eukaryotic protein kinase domain
 - Location within SEQ ID NO 2665: from 1 to 134 aa.

- (D) Related Amino Acid Sequences
 - Alignment No. 16321
 - gi No. 1169128
 - % Identity 70.8
 - Alignment Length 137
 - Location of Alignment in SEQ ID NO 2665: from 3 to 139
 - Alignment No. 16322
 - gi No. 2253010
 - % Identity 74
 - Alignment Length 154
 - Location of Alignment in SEQ ID NO 2665: from 1 to 154
 - Alignment No. 16323
 - qi No. 3063459
 - % Identity 86.9
 - Alignment Length 145
 - Location of Alignment in SEQ ID NO 2665: from 1 to 145
 - Alignment No. 16324
 - gi No. 3201541
 - % Identity 87.6
 - Alignment Length 145
 - Location of Alignment in SEQ ID NO 2665: from 1 to 145
 - Alignment No. 16325
 - gi No. 322577
 - % Identity 70.8
 - Alignment Length 137
 - Location of Alignment in SEQ ID NO 2665: from 3 to 139
- (B) Polypeptide Sequence
 - Pat. Appln. SEQ ID NO 2666
 - Ceres seq_id 1504186
 - Location of start within SEQ ID NO 2664: at 6 nt.
- (C) Nomination and Annotation of Domains within Predicted Polypeptide(s)
 - Alignment No. 16326
 - Eukaryotic protein kinase domain
 - Location within SEQ ID NO 2666: from 1 to 133 aa.
 - (D) Related Amino Acid Sequences
 - Alignment No. 16327
 - gi No. 1169128
 - % Identity 70.8
 - Alignment Length 137
 - Location of Alignment in SEQ ID NO 2666: from 2 to 138
 - Alignment No. 16328
 - gi No. 2253010
 - % Identity 74
 - Alignment Length 154
 - Location of Alignment in SEQ ID NO 2666: from 1 to 153
 - Alignment No. 16329
 - gi No. 3063459
 - % Identity 86.9
 - Alignment Length 145
 - Location of Alignment in SEQ ID NO 2666: from 1 to 144

- Alignment No. 16330
- gi No. 3201541
- % Identity 87.6
- Alignment Length 145
- Location of Alignment in SEQ ID NO 2666: from 1 to 144
- Alignment No. 16331
- qi No. 322577
- % Identity 70.8
- Alignment Length 137
- Location of Alignment in SEQ ID NO 2666: from 2 to 138
- (B) Polypeptide Sequence
 - Pat. Appln. SEQ ID NO 2667
 - Ceres seq_id 1504187
 - Location of start within SEQ ID NO 2664: at 153 nt.
- - Alignment No. 16332
 - Eukaryotic protein kinase domain
 - Location within SEQ ID NO 2667: from 1 to 84 aa.
 - (D) Related Amino Acid Sequences
 - Alignment No. 16333
 - gi No. 1169128
 - % Identity 70.8
 - Alignment Length 137
 - Location of Alignment in SEQ ID NO 2667: from 1 to 89
 - Alignment No. 16334
 - gi No. 2253010
 - % Identity 74
 - Alignment Length 154
 - Location of Alignment in SEQ ID NO 2667: from 1 to 104
 - Alignment No. 16335
 - gi No. 3063459
 - % Identity 86.9
 - Alignment Length 145
 - Location of Alignment in SEQ ID NO 2667: from 1 to 95
 - Alignment No. 16336
 - gi No. 3201541
 - % Identity 87.6
 - Alignment Length 145
 - Location of Alignment in SEQ ID NO 2667: from 1 to 95
 - Alignment No. 16337
 - gi No. 322577
 - % Identity 70.8
 - Alignment Length 137
 - Location of Alignment in SEQ ID NO 2667: from 1 to 89

- (A) Polynucleotide Sequence
 - Pat. Appln. SEQ ID NO 2668
 - Ceres seq_id 1504192
 - (B) Polypeptide Sequence
 - Pat. Appln. SEQ ID NO 2669

- Ceres seq id 1504193
- Location of start within SEQ ID NO 2668: at 3 nt.
- (C) Nomination and Annotation of Domains within Predicted Polypeptide(s)
 - (D) Related Amino Acid Sequences
 - Alignment No. 16338
 - gi No. 5042432
 - % Identity 70.6
 - Alignment Length 68
 - Location of Alignment in SEQ ID NO 2669: from 93 to 159
 - (B) Polypeptide Sequence
 - Pat. Appln. SEQ ID NO 2670
 - Ceres seq_id 1504194
 - Location of start within SEQ ID NO 2668: at 87 nt.
- (C) Nomination and Annotation of Domains within Predicted Polypeptide(s)
 - (D) Related Amino Acid Sequences
 - Alignment No. 16339
 - gi No. 5042432
 - % Identity 70.6
 - Alignment Length 68
 - Location of Alignment in SEQ ID NO 2670: from 65 to 131

- (A) Polynucleotide Sequence
 - Pat. Appln. SEQ ID NO 2671
 - Ceres seq_id 1504201
 - (B) Polypeptide Sequence
 - Pat. Appln. SEQ ID NO 2672
 - Ceres seq_id 1504202
 - Location of start within SEQ ID NO 2671: at 3 nt.
- (C) Nomination and Annotation of Domains within Predicted Polypeptide(s)
 - (D) Related Amino Acid Sequences
 - (B) Polypeptide Sequence
 - Pat. Appln. SEQ ID NO 2673
 - Ceres seq_id 1504203
 - Location of start within SEQ ID NO 2671: at 369 nt.
- (C) Nomination and Annotation of Domains within Predicted Polypeptide(s)
 - (D) Related Amino Acid Sequences
 - Alignment No. 16340
 - gi No. 2642447
 - % Identity 76
 - Alignment Length 25
 - Location of Alignment in SEQ ID NO 2673: from 23 to 46
 - Alignment No. 16341

 - gi No. 4335730
 % Identity 76.9
 - Alignment Length 26
 - Location of Alignment in SEQ ID NO 2673: from 22 to 46
 - Alignment No. 16342
 - gi No. 4544385

- % Identity 76
- Alignment Length 25
- Location of Alignment in SEQ ID NO 2673: from 23 to 46
- (B) Polypeptide Sequence
 - Pat. Appln. SEQ ID NO 2674
 - Ceres seq_id 1504204
 - Location of start within SEQ ID NO 2671: at 378 nt.
- (C) Nomination and Annotation of Domains within Predicted Polypeptide(s)
 - (D) Related Amino Acid Sequences
 - Alignment No. 16343
 - gi No. 2642447
 - % Identity 76
 - Alignment Length 25
 - Location of Alignment in SEQ ID NO 2674: from 20 to 43
 - Alignment No. 16344
 - gi No. 4335730
 - % Identity 76.9
 - Alignment Length 26
 - Location of Alignment in SEQ ID NO 2674: from 19 to 43
 - Alignment No. 16345
 - gi No. 4544385
 - % Identity 76
 - Alignment Length 25
 - Location of Alignment in SEQ ID NO 2674: from 20 to 43

- (A) Polynucleotide Sequence
 - Pat. Appln. SEQ ID NO 2675
 - Ceres seq_id 1504231
 - (B) Polypeptide Sequence
 - Pat. Appln. SEQ ID NO 2676
 - Ceres seq_id 1504232
 - Location of start within SEQ ID NO 2675: at 2 nt.
- (C) Nomination and Annotation of Domains within Predicted Polypeptide(s)
 - (D) Related Amino Acid Sequences
 - Alignment No. 16346
 - gi No. 1076389
 - % Identity 93.8
 - Alignment Length 145
 - Location of Alignment in SEQ ID NO 2676: from 1 to 144
 - Alignment No. 16347
 - gi No. 1076390
 - % Identity 95.2
 - Alignment Length 145
 - Location of Alignment in SEQ ID NO 2676: from 1 to 144
 - Alignment No. 16348
 - gi No. 1076396
 - % Identity 92.4
 - Alignment Length 145
 - Location of Alignment in SEQ ID NO 2676: from 1 to 144
 - Alignment No. 16349

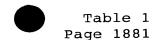
- gi No. 1262171 - % Identity 92.4 - Alignment Length 145 - Location of Alignment in SEQ ID NO 2676: from 1 to 144 - Alignment No. 16350 - gi No. 1568511 - % Identity 94.5 - Alignment Length 145 - Location of Alignment in SEQ ID NO 2676: from 1 to 144 - Alignment No. 16351 - gi No. 2129734 - % Identity 92.4 - Alignment Length 145 - Location of Alignment in SEQ ID NO 2676: from 1 to 144 - Alignment No. 16352 - gi No. 2146743 - % Identity 92.4 - Alignment Length 145 - Location of Alignment in SEQ ID NO 2676: from 1 to 144 - Alignment No. 16353 - gi No. 261767 - % Identity 76.2 - Alignment Length 21 - Location of Alignment in SEQ ID NO 2676: from 125 to 144 - Alignment No. 16354 - gi No. 3928142 - % Identity 93.8 - Alignment Length 145 - Location of Alignment in SEQ ID NO 2676: from 1 to 144 - Alignment No. 16355 - gi No. 476923 - % Identity 76.2 - Alignment Length 21 - Location of Alignment in SEQ ID NO 2676: from 125 to 144 - Alignment No. 16356 - gi No. 543715 - % Identity 90.3 - Alignment Length 145 - Location of Alignment in SEQ ID NO 2676: from 1 to 144 - Alignment No. 16357 - gi No. 5679684 - % Identity 93.8 - Alignment Length 145 - Location of Alignment in SEQ ID NO 2676: from 1 to 144 - Alignment No. 16358

- Location of Alignment in SEQ ID NO 2676: from 1 to 144

(B) Polypeptide SequencePat. Appln. SEQ ID NO 2677

- gi No. 683506
- % Identity 91.7
- Alignment Length 145

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- Ceres seq_id 1504233
- Location of start within SEQ ID NO 2675: at 44 nt.
- (C) Nomination and Annotation of Domains within Predicted Polypeptide(s)
 - (D) Related Amino Acid Sequences
 - Alignment No. 16359
 - gi No. 1076389
 - % Identity 93.8
 - Alignment Length 145
 - Location of Alignment in SEQ ID NO 2677: from 1 to 130
 - Alignment No. 16360
 - gi No. 1076390
 - % Identity 95.2
 - Alignment Length 145
 - Location of Alignment in SEQ ID NO 2677: from 1 to 130
 - Alignment No. 16361
 - gi No. 1076396
 - % Identity 92.4
 - Alignment Length 145
 - Location of Alignment in SEQ ID NO 2677: from 1 to 130
 - Alignment No. 16362
 - gi No. 1262171
 - % Identity 92.4
 - Alignment Length 145
 - Location of Alignment in SEQ ID NO 2677: from 1 to 130
 - Alignment No. 16363
 - gi No. 1568511
 - % Identity 94.5
 - Alignment Length 145
 - Location of Alignment in SEQ ID NO 2677: from 1 to 130
 - Alignment No. 16364
 - gi No. 2129734
 - % Identity 92.4
 - Alignment Length 145
 - Location of Alignment in SEQ ID NO 2677: from 1 to 130
 - Alignment No. 16365
 - gi No. 2146743
 - % Identity 92.4
 - Alignment Length 145
 - Location of Alignment in SEQ ID NO 2677: from 1 to 130
 - Alignment No. 16366
 - gi No. 261767
 - % Identity 76.2
 - Alignment Length 21
 - Location of Alignment in SEQ ID NO 2677: from 111 to 130
 - Alignment No. 16367
 - gi No. 3928142
 - % Identity 93.8
 - Alignment Length 145
 - Location of Alignment in SEQ ID NO 2677: from 1 to 130
 - Alignment No. 16368

- gi No. 476923
- % Identity 76.2
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2677: from 111 to 130
- Alignment No. 16369
- gi No. 543715
- % Identity 90.3
- Alignment Length 145
- Location of Alignment in SEQ ID NO 2677: from 1 to 130
- Alignment No. 16370
- gi No. 5679684
- % Identity 93.8
- Alignment Length 145
- Location of Alignment in SEQ ID NO 2677: from 1 to 130
- Alignment No. 16371
- gi No. 683506
- % Identity 91.7
- Alignment Length 145
- Location of Alignment in SEQ ID NO 2677: from 1 to 130

- (A) Polynucleotide Sequence
 - Pat. Appln. SEQ ID NO 2678
 - Ceres seq id 1504239
 - (B) Polypeptide Sequence
 - Pat. Appln. SEQ ID NO 2679
 - Ceres seq_id 1504240
 - Location of start within SEQ ID NO 2678: at 2 nt.
- (C) Nomination and Annotation of Domains within Predicted Polypeptide(s)
 - Alignment No. 16372
 - PCI domain
 - Location within SEQ ID NO 2679: from 7 to 86 aa.
 - (D) Related Amino Acid Sequences

- (A) Polynucleotide Sequence
 - Pat. Appln. SEQ ID NO 2680
 - Ceres seq_id 1504254
 - (B) Polypeptide Sequence
 - Pat. Appln. SEQ ID NO 2681
 - Ceres seq_id 1504255
 - Location of start within SEQ ID NO 2680: at 3 nt.
- - (D) Related Amino Acid Sequences
 - Alignment No. 16373
 - gi No. 1076294
 - % Identity 81.3
 - Alignment Length 16
 - Location of Alignment in SEQ ID NO 2681: from 92 to 107
 - Alignment No. 16374
 - gi No. 1279640
 - % Identity 71.1

- Alignment Length 45
- Location of Alignment in SEQ ID NO 2681: from 64 to 107
- Alignment No. 16375
- gi No. 1321924
- % Identity 71.1
- Alignment Length 45
- Location of Alignment in SEQ ID NO 2681: from 64 to 107
- Alignment No. 16376
- gi No. 1944132
- % Identity 71.1
- Alignment Length 45
- Location of Alignment in SEQ ID NO 2681: from 64 to 107
- Alignment No. 16377
- gi No. 4972066
- % Identity 73.7
- Alignment Length 19
- Location of Alignment in SEQ ID NO 2681: from 89 to 107
- Alignment No. 16378
- gi No. 5679845
- % Identity 70
- Alignment Length 20
- Location of Alignment in SEQ ID NO 2681: from 89 to 107
- (B) Polypeptide Sequence
 - Pat. Appln. SEQ ID NO 2682
 - Ceres seq_id 1504256
 - Location of start within SEQ ID NO 2680: at 91 nt.
- (C) Nomination and Annotation of Domains within Predicted Polypeptide(s)
 - (D) Related Amino Acid Sequences
 - Alignment No. 16379
 - gi No. 1279640
 - % Identity 81.8
 - Alignment Length 22
 - Location of Alignment in SEQ ID NO 2682: from 11 to 32
 - Alignment No. 16380
 - gi No. 1321924
 - % Identity 81.8
 - Alignment Length 22
 - Location of Alignment in SEQ ID NO 2682: from 11 to 32
 - Alignment No. 16381
 - gi No. 1944132
 - % Identity 90.9
 - Alignment Length 22
 - Location of Alignment in SEQ ID NO 2682: from 11 to 32
 - Alignment No. 16382
 - gi No. 2894607
 - % Identity 81.8
 - Alignment Length 22
 - Location of Alignment in SEQ ID NO 2682: from 11 to 32
 - Alignment No. 16383
 - gi No. 4585977

- % Identity 75
- Alignment Length 24
- Location of Alignment in SEQ ID NO 2682: from 9 to 32
- Alignment No. 16384
- gi No. 5091624
- % Identity 75
- Alignment Length 20
- Location of Alignment in SEQ ID NO 2682: from 13 to 32
- Alignment No. 16385
- gi No. 5091626
- % Identity 75
- Alignment Length 20
- Location of Alignment in SEQ ID NO 2682: from 13 to 32
- Alignment No. 16386
- gi No. 5306267
- % Identity 70
- Alignment Length 20
- Location of Alignment in SEQ ID NO 2682: from 13 to 32
- Alignment No. 16387
- gi No. 5679845
- % Identity 72.7
- Alignment Length 22
- Location of Alignment in SEQ ID NO 2682: from 11 to 32
- (B) Polypeptide Sequence
 - Pat. Appln. SEQ ID NO 2683
 - Ceres seq_id 1504257
 - Location of start within SEQ ID NO 2680: at 115 nt.
- (C) Nomination and Annotation of Domains within Predicted Polypeptide(s)
 - (D) Related Amino Acid Sequences
 - Alignment No. 16388
 - gi No. 1279640
 - % Identity 81.8
 - Alignment Length 22
 - Location of Alignment in SEQ ID NO 2683: from 3 to 24
 - Alignment No. 16389
 - gi No. 1321924
 - % Identity 81.8
 - Alignment Length 22
 - Location of Alignment in SEQ ID NO 2683: from 3 to 24
 - Alignment No. 16390
 - gi No. 1944132
 - % Identity 90.9
 - Alignment Length 22
 - Location of Alignment in SEQ ID NO 2683: from 3 to 24
 - Alignment No. 16391
 - gi No. 2894607
 - % Identity 81.8
 - Alignment Length 22
 - Location of Alignment in SEQ ID NO 2683: from 3 to 24
 - Alignment No. 16392

- gi No. 4585977
- % Identity 75
- Alignment Length 24
- Location of Alignment in SEQ ID NO 2683: from 1 to 24
- Alignment No. 16393
- gi No. 5091624
- % Identity 75
- Alignment Length 20
- Location of Alignment in SEQ ID NO 2683: from 5 to 24
- Alignment No. 16394
- gi No. 5091626
- % Identity 75
- Alignment Length 20
- Location of Alignment in SEQ ID NO 2683: from 5 to 24
- Alignment No. 16395
- gi No. 5306267
- % Identity 70
- Alignment Length 20
- Location of Alignment in SEQ ID NO 2683: from 5 to 24
- Alignment No. 16396
- gi No. 5679845
- % Identity 72.7
- Alignment Length 22
- Location of Alignment in SEQ ID NO 2683: from 3 to 24

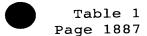
- (A) Polynucleotide Sequence
 - Pat. Appln. SEQ ID NO 2684
 - Ceres seq_id 1504258
 - (B) Polypeptide Sequence
 - Pat. Appln. SEQ ID NO 2685
 - Ceres seq_id 1504259
 - Location of start within SEQ ID NO 2684: at 1 nt.
- - (D) Related Amino Acid Sequences
 - (B) Polypeptide Sequence
 - Pat. Appln. SEQ ID NO 2686
 - Ceres seq_id 1504260
 - Location of start within SEQ ID NO 2684: at 2 nt.
- - (D) Related Amino Acid Sequences
 - (B) Polypeptide Sequence
 - Pat. Appln. SEQ ID NO 2687
 - Ceres seq_id 1504261
 - Location of start within SEQ ID NO 2684: at 195 nt.
- (C) Nomination and Annotation of Domains within Predicted Polypeptide(s)
 - (D) Related Amino Acid Sequences
 - Alignment No. 16397
 - gi No. 2642154

- % Identity 74.3
- Alignment Length 35
- Location of Alignment in SEQ ID NO 2687: from 1 to 35

- (A) Polynucleotide Sequence
 - Pat. Appln. SEQ ID NO 2688
 - Ceres seq_id 1504270
 - (B) Polypeptide Sequence
 - Pat. Appln. SEQ ID NO 2689
 - Ceres seq_id 1504271
 - Location of start within SEQ ID NO 2688: at 1 nt.
- (C) Nomination and Annotation of Domains within Predicted Polypeptide(s)
 - (D) Related Amino Acid Sequences
 - (B) Polypeptide Sequence
 - Pat. Appln. SEQ ID NO 2690
 - Ceres seq_id 1504272
 - Location of start within SEQ ID NO 2688: at 2 nt.
- (C) Nomination and Annotation of Domains within Predicted Polypeptide(s)
 - (D) Related Amino Acid Sequences
 - Alignment No. 16398
 - gi No. 1546779
 - % Identity 75
 - Alignment Length 12
 - Location of Alignment in SEQ ID NO 2690: from 21 to 32
 - Alignment No. 16399
 - gi No. 2136108
 - % Identity 75
 - Alignment Length 12
 - Location of Alignment in SEQ ID NO 2690: from 21 to 32
 - Alignment No. 16400
 - gi No. 3858885
 - % Identity 75
 - Alignment Length 12
 - Location of Alignment in SEQ ID NO 2690: from 21 to 32
 - (B) Polypeptide Sequence
 - Pat. Appln. SEQ ID NO 2691
 - Ceres seq_id 1504273
 - Location of start within SEQ ID NO 2688: at 3 nt.
- (C) Nomination and Annotation of Domains within Predicted Polypeptide(s)
 - (D) Related Amino Acid Sequences

- (A) Polynucleotide Sequence
 - Pat. Appln. SEQ ID NO 2692
 - Ceres seq_id 1504274
 - (B) Polypeptide Sequence
 - Pat. Appln. SEQ ID NO 2693
 - Ceres seq_id 1504275
 - Location of start within SEQ ID NO 2692: at 2 nt.

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- (C) Nomination and Annotation of Domains within Predicted Polypeptide(s)
 - Alignment No. 16401
 - Metallothionein
 - Location within SEQ ID NO 2693: from 37 to 88 aa.
 - (D) Related Amino Acid Sequences
 - Alignment No. 16402
 - gi No. 1944205
 - % Identity 73
 - Alignment Length 37
 - Location of Alignment in SEQ ID NO 2693: from 37 to 73
 - Alignment No. 16403
 - qi No. 225131
 - % Identity 70
 - Alignment Length 21
 - Location of Alignment in SEQ ID NO 2693: from 40 to 59
 - Alignment No. 16404
 - qi No. 225144
 - % Identity 71.4
 - Alignment Length 22
 - Location of Alignment in SEQ ID NO 2693: from 39 to 59
 - Alignment No. 16405
 - gi No. 225146
 - % Identity 70
 - Alignment Length 21
 - Location of Alignment in SEQ ID NO 2693: from 40 to 59
 - Alignment No. 16406
 - gi No. 2407285
 - % Identity 70.3
 - Alignment Length 37
 - Location of Alignment in SEQ ID NO 2693: from 37 to 73
 - Alignment No. 16407
 - gi No. 2497897
 - % Identity 70.8
 - Alignment Length 48
 - Location of Alignment in SEQ ID NO 2693: from 37 to 84
 - Alignment No. 16408
 - gi No. 2497903
 - % Identity 76.9
 - Alignment Length 52
 - Location of Alignment in SEQ ID NO 2693: from 37 to 88
 - Alignment No. 16409
 - gi No. 2662415
 - % Identity 72.5
 - Alignment Length 52
 - Location of Alignment in SEQ ID NO 2693: from 38 to 88
 - Alignment No. 16410
 - gi No. 2815246
 - % Identity 74.5
 - Alignment Length 47
 - Location of Alignment in SEQ ID NO 2693: from 37 to 83

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- Alignment No. 16411
- gi No. 541943
- % Identity 75
- Alignment Length 48
- Location of Alignment in SEQ ID NO 2693: from 37 to 84
- (B) Polypeptide Sequence
 - Pat. Appln. SEQ ID NO 2694
 - Ceres seq id 1504276
 - Location of start within SEQ ID NO 2692: at 110 nt.
- (C) Nomination and Annotation of Domains within Predicted Polypeptide(s)
 - Alignment No. 16412
 - Metallothionein
 - Location within SEQ ID NO 2694: from 1 to 52 aa.
 - (D) Related Amino Acid Sequences
 - Alignment No. 16413
 - gi No. 1944205
 - % Identity 73
 - Alignment Length 37
 - Location of Alignment in SEQ ID NO 2694: from 1 to 37
 - Alignment No. 16414
 - gi No. 225131
 - % Identity 70
 - Alignment Length 21
 - Location of Alignment in SEQ ID NO 2694: from 4 to 23
 - Alignment No. 16415
 - gi No. 225144
 - % Identity 71.4
 - Alignment Length 22
 - Location of Alignment in SEQ ID NO 2694: from 3 to 23
 - Alignment No. 16416
 - gi No. 225146
 - % Identity 70
 - Alignment Length 21
 - Location of Alignment in SEQ ID NO 2694: from 4 to 23
 - Alignment No. 16417
 - gi No. 2407285
 - % Identity 70.3
 - Alignment Length 37
 - Location of Alignment in SEQ ID NO 2694: from 1 to 37
 - Alignment No. 16418
 - qi No. 2497897
 - % Identity 70.8
 - Alignment Length 48
 - Location of Alignment in SEQ ID NO 2694: from 1 to 48
 - Alignment No. 16419
 - gi No. 2497903
 - % Identity 76.9
 - Alignment Length 52
 - Location of Alignment in SEQ ID NO 2694: from 1 to 52
 - Alignment No. 16420

- gi No. 2662415
 % Identity 72.5
- Alignment Length 52
- Location of Alignment in SEQ ID NO 2694: from 2 to 52
- Alignment No. 16421
- gi No. 2815246
- % Identity 74.5
- Alignment Length 47
- Location of Alignment in SEQ ID NO 2694: from 1 to 47
- Alignment No. 16422
- gi No. 541943
- % Identity 75
- Alignment Length 48
- Location of Alignment in SEQ ID NO 2694: from 1 to 48

- (A) Polynucleotide Sequence
 - Pat. Appln. SEQ ID NO 2695
 - Ceres seq_id 1504277
 - (B) Polypeptide Sequence
 - Pat. Appln. SEQ ID NO 2696
 - Ceres seq_id 1504278
 - Location of start within SEQ ID NO 2695: at 2 nt.
- - (D) Related Amino Acid Sequences
 - Alignment No. 16423
 - gi No. 2145062
 - % Identity 72.7
 - Alignment Length 11
 - Location of Alignment in SEQ ID NO 2696: from 70 to 80
 - (B) Polypeptide Sequence
 - Pat. Appln. SEQ ID NO 2697
 - Ceres seq_id 1504279
 - Location of start within SEQ ID NO 2695: at 3 nt.
- (C) Nomination and Annotation of Domains within Predicted Polypeptide(s)
 - Alignment No. 16424
 - Collagen triple helix repeat (20 copies)
 - Location within SEQ ID NO 2697: from 7 to 57 aa.
 - (D) Related Amino Acid Sequences
 - Alignment No. 16425
 - gi Ño. 1042189
 - % Identity 83.3
 - Alignment Length 12
 - Location of Alignment in SEQ ID NO 2697: from 27 to 38
 - Alignment No. 16426
 - gi No. 1042189
 - % Identity 83.3
 - Alignment Length 12
 - Location of Alignment in SEQ ID NO 2697: from 27 to 38
 - Alignment No. 16427
 - gi No. 131036

- % Identity 83.3
- Alignment Length 12
- Location of Alignment in SEQ ID NO 2697: from 27 to 38
- Alignment No. 16428
- gi No. 131036
- % Identity 83.3
- Alignment Length 12
- Location of Alignment in SEQ ID NO 2697: from 27 to 38
- Alignment No. 16429
- gi No. 1703594
- % Identity 72.7
- Alignment Length 11
- Location of Alignment in SEQ ID NO 2697: from 3 to 13
- Alignment No. 16430
- gi No. 2134213
- % Identity 72.7
- Alignment Length 11
- Location of Alignment in SEQ ID NO 2697: from 27 to 37
- Alignment No. 16431
- gi No. 2134213
- % Identity 91.7
- Alignment Length 12
- Location of Alignment in SEQ ID NO 2697: from 27 to 38
- Alignment No. 16432
- gi No. 2134213
- % Identity 78.6
- Alignment Length 14
- Location of Alignment in SEQ ID NO 2697: from 25 to 38
- Alignment No. 16433
- gi No. 2498095
- % Identity 75
- Alignment Length 12
- Location of Alignment in SEQ ID NO 2697: from 27 to 38
- Alignment No. 16434
- gi No. 462338
- % Identity 75
- Alignment Length 12
- Location of Alignment in SEQ ID NO 2697: from 27 to 38
- Alignment No. 16435
- gi No. 462338
- % Identity 76.9
- Alignment Length 13
- Location of Alignment in SEQ ID NO 2697: from 27 to 38
- (B) Polypeptide Sequence
 - Pat. Appln. SEQ ID NO 2698
 - Ceres seq_id 1504280
 - Location of start within SEQ ID NO 2695: at 119 nt.
- (C) Nomination and Annotation of Domains within Predicted Polypeptide(s)
 - (D) Related Amino Acid Sequences
 - Alignment No. 16436

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- qi No. 2145062
- % Identity 72.7
- Alignment Length 11
- Location of Alignment in SEQ ID NO 2698: from 31 to 41

- (A) Polynucleotide Sequence
 - Pat. Appln. SEQ ID NO 2699
 - Ceres seq_id 1504299
 - (B) Polypeptide Sequence
 - Pat. Appln. SEQ ID NO 2700
 - Ceres seq_id 1504300
 - Location of start within SEQ ID NO 2699: at 1 nt.
- - Alignment No. 16437
 - Chitin recognition protein
 - Location within SEQ ID NO 2700: from 42 to 76 aa.
 - (D) Related Amino Acid Sequences
 - Alignment No. 16438
 - gi No. 116329
 - % Identity 71.2
 - Alignment Length 53
 - Location of Alignment in SEQ ID NO 2700: from 26 to 76
 - Alignment No. 16439
 - gi No. 283037
 - % Identity 71.2
 - Alignment Length 53
 - Location of Alignment in SEQ ID NO 2700: from 26 to 76
 - (B) Polypeptide Sequence
 - Pat. Appln. SEQ ID NO 2701
 - Ceres seq_id 1504301
 - Location of start within SEQ ID NO 2699: at 34 nt.
- - Alignment No. 16440
 - Chitin recognition protein
 - Location within SEQ ID NO 2701: from 31 to 65 aa.
 - (D) Related Amino Acid Sequences
 - Alignment No. 16441
 - gi No. 116329
 - % Identity 71.2
 - Alignment Length 53
 - Location of Alignment in SEQ ID NO 2701: from 15 to 65
 - Alignment No. 16442
 - gi No. 283037
 - % Identity 71.2
 - Alignment Length 53
 - Location of Alignment in SEQ ID NO 2701: from 15 to 65
 - (B) Polypeptide Sequence
 - Pat. Appln. SEQ ID NO 2702
 - Ceres seq_id 1504302
 - Location of start within SEQ ID NO 2699: at 40 nt.

- (C) Nomination and Annotation of Domains within Predicted Polypeptide(s)
 - Alignment No. 16443
 - Chitin recognition protein
 - Location within SEQ ID NO 2702: from 29 to 63 aa.
 - (D) Related Amino Acid Sequences
 - Alignment No. 16444
 - gi No. 116329
 - % Identity 71.2
 - Alignment Length 53
 - Location of Alignment in SEQ ID NO 2702: from 13 to 63
 - Alignment No. 16445
 - gi No. 283037
 - % Identity 71.2
 - Alignment Length 53
 - Location of Alignment in SEQ ID NO 2702: from 13 to 63

- (A) Polynucleotide Sequence
 - Pat. Appln. SEQ ID NO 2703
 - Ceres seq_id 1504303
 - (B) Polypeptide Sequence
 - Pat. Appln. SEQ ID NO 2704
 - Ceres seq_id 1504304
 - Location of start within SEQ ID NO 2703: at 1 nt.
- - Alignment No. 16446
 - PCI domain
 - Location within SEQ ID NO 2704: from 99 to 149 aa.
 - (D) Related Amino Acid Sequences
 - (B) Polypeptide Sequence
 - Pat. Appln. SEQ ID NO 2705
 - Ceres seq_id 1504305
 - Location of start within SEQ ID NO 2703: at 106 nt.
- (C) Nomination and Annotation of Domains within Predicted Polypeptide(s)
 - Alignment No. 16447
 - PCI domain
 - Location within SEQ ID NO 2705: from 64 to 114 aa.
 - (D) Related Amino Acid Sequences
 - (B) Polypeptide Sequence
 - Pat. Appln. SEQ ID NO 2706
 - Ceres seq_id 1504306
 - Location of start within SEQ ID NO 2703: at 196 nt.
- - Alignment No. 16448
 - PCI domain
 - Location within SEQ ID NO 2706: from 34 to 84 aa.

(D) Related Amino Acid Sequences

- (A) Polynucleotide Sequence
 - Pat. Appln. SEQ ID NO 2707
 - Ceres seq_id 1504307
 - (B) Polypeptide Sequence
 - Pat. Appln. SEQ ID NO 2708
 - Ceres seq_id 1504308
 - Location of start within SEQ ID NO 2707: at 3 nt.
- - (D) Related Amino Acid Sequences
 - (B) Polypeptide Sequence
 - Pat. Appln. SEQ ID NO 2709
 - Ceres seq_id 1504309
 - Location of start within SEQ ID NO 2707: at 83 nt.
- (C) Nomination and Annotation of Domains within Predicted Polypeptide(s)
 - (D) Related Amino Acid Sequences
 - Alignment No. 16449
 - gi No. 133902
 - % Identity 76.6
 - Alignment Length 47
 - Location of Alignment in SEQ ID NO 2709: from 8 to 54
 - Alignment No. 16450
 - gi No. 1350971
 - % Identity 88.9
 - Alignment Length 54
 - Location of Alignment in SEQ ID NO 2709: from 1 to 54
 - Alignment No. 16451
 - gi No. 1350972
 - % Identity 76.6
 - Alignment Length 47
 - Location of Alignment in SEQ ID NO 2709: from 8 to 54
 - Alignment No. 16452
 - gi No. 2078466
 - % Identity 74.5
 - Alignment Length 47
 - Location of Alignment in SEQ ID NO 2709: from 8 to 54
 - Alignment No. 16453
 - gi No. 2500501
 - % Identity 96.3
 - Alignment Length 54
 - Location of Alignment in SEQ ID NO 2709: from 1 to 54
 - Alignment No. 16454
 - qi No. 2979561
 - % Identity 92.6
 - Alignment Length 54
 - Location of Alignment in SEQ ID NO 2709: from 1 to 54
 - Alignment No. 16455
 - gi No. 3098456

- % Identity 72.7
- Alignment Length 44
- Location of Alignment in SEQ ID NO 2709: from 11 to 54
- Alignment No. 16456
- gi No. 4038471
- % Identity 98.1
- Alignment Length 54
- Location of Alignment in SEQ ID NO 2709: from 1 to 54
- Alignment No. 16457
- qi No. 4193382
- % Identity 92.6
- Alignment Length 54
- Location of Alignment in SEQ ID NO 2709: from 1 to 54
- Alignment No. 16458
- gi No. 4321094
- % Identity 70.8
- Alignment Length 48
- Location of Alignment in SEQ ID NO 2709: from 7 to 54
- Alignment No. 16459
- gi No. 4432748
- % Identity 76.6
- Alignment Length 47
- Location of Alignment in SEQ ID NO 2709: from 8 to 54
- Alignment No. 16460
- gi No. 4506711
- % Identity 76.6
- Alignment Length 47
- Location of Alignment in SEQ ID NO 2709: from 8 to 54
- (B) Polypeptide Sequence
 - Pat. Appln. SEQ ID NO 2710
 - Ceres seq_id 1504310
 - Location of start within SEQ ID NO 2707: at 185 nt.
- - (D) Related Amino Acid Sequences
 - Alignment No. 16461
 - gi No. 133902
 - % Identity 76.6
 - Alignment Length 47
 - Location of Alignment in SEQ ID NO 2710: from 1 to 20
 - Alignment No. 16462
 - gi No. 1350971
 - % Identity 88.9
 - Alignment Length 54
 - Location of Alignment in SEQ ID NO 2710: from 1 to 20
 - Alignment No. 16463
 - gi No. 1350972
 - % Identity 76.6
 - Alignment Length 47
 - Location of Alignment in SEQ ID NO 2710: from 1 to 20
 - Alignment No. 16464

- gi No. 2078466% Identity 74.5Alignment Length 47
- Location of Alignment in SEQ ID NO 2710: from 1 to 20
- Alignment No. 16465
- gi No. 2500501
- % Identity 96.3
- Alignment Length 54
- Location of Alignment in SEQ ID NO 2710: from 1 to 20
- Alignment No. 16466
- gi No. 2979561
- % Identity 92.6
- Alignment Length 54
- Location of Alignment in SEQ ID NO 2710: from 1 to 20
- Alignment No. 16467
- gi No. 3098456
- % Identity 72.7
- Alignment Length 44
- Location of Alignment in SEQ ID NO 2710: from 1 to 20
- Alignment No. 16468
- gi No. 4038471
- % Identity 98.1
- Alignment Length 54
- Location of Alignment in SEQ ID NO 2710: from 1 to 20
- Alignment No. 16469
- gi No. 4193382
- % Identity 92.6
- Alignment Length 54
- Location of Alignment in SEQ ID NO 2710: from 1 to 20
- Alignment No. 16470
- gi No. 4321094
- % Identity 70.8
- Alignment Length 48
- Location of Alignment in SEQ ID NO 2710: from 1 to 20
- Alignment No. 16471
- gi No. 4432748
- % Identity 76.6
- Alignment Length 47
- Location of Alignment in SEQ ID NO 2710: from 1 to 20
- Alignment No. 16472
- gi No. 4506711
- % Identity 76.6
- Alignment Length 47
- Location of Alignment in SEQ ID NO 2710: from 1 to 20

- (A) Polynucleotide Sequence
 - Pat. Appln. SEQ ID NO 2711
 - Ceres seq_id 1504311
 - (B) Polypeptide Sequence
 - Pat. Appln. SEQ ID NO 2712
 - Ceres seq_id 1504312
 - Location of start within SEQ ID NO 2711: at 3 nt.

- (C) Nomination and Annotation of Domains within Predicted Polypeptide(s)
 - (D) Related Amino Acid Sequences
 - (B) Polypeptide Sequence
 - Pat. Appln. SEQ ID NO 2713
 - Ceres seq id 1504313
 - Location of start within SEQ ID NO 2711: at 118 nt.
- (C) Nomination and Annotation of Domains within Predicted Polypeptide(s)
 - (D) Related Amino Acid Sequences
 - Alignment No. 16473
 - gi No. 100789
 - % Identity 70.5
 - Alignment Length 45
 - Location of Alignment in SEQ ID NO 2713: from 1 to 43
 - Alignment No. 16474
 - gi No. 100883
 - % Identity 93.2
 - Alignment Length 44
 - Location of Alignment in SEQ ID NO 2713: from 1 to 43
 - Alignment No. 16475
 - gi No. 1122313

 - % Identity 79.5 Alignment Length 44
 - Location of Alignment in SEQ ID NO 2713: from 1 to 43
 - Alignment No. 16476
 - gi No. 1122315
 - % Identity 75
 - Alignment Length 44
 - Location of Alignment in SEQ ID NO 2713: from 1 to 43
 - Alignment No. 16477
 - gi No. 123541
 - % Identity 77.8
 - Alignment Length 18
 - Location of Alignment in SEQ ID NO 2713: from 5 to 22
 - Alignment No. 16478
 - gi No. 123545
 - % Identity 70.5
 - Alignment Length 45
 - Location of Alignment in SEQ ID NO 2713: from 1 to 43
 - Alignment No. 16479
 - gi No. 123546
 - % Identity 72.2
 - Alignment Length 18
 - Location of Alignment in SEQ ID NO 2713: from 5 to 22
 - Alignment No. 16480
 - gi No. 1536911
 - % Identity 75
 - Alignment Length 45
 - Location of Alignment in SEQ ID NO 2713: from 1 to 43

- Alignment No. 16481
- qi No. 232272
- % Identity 70.6
- Alignment Length 17
- Location of Alignment in SEQ ID NO 2713: from 5 to 21
- Alignment No. 16482
- gi No. 445136
- % Identity 70.5
- Alignment Length 45
- Location of Alignment in SEQ ID NO 2713: from 1 to 43
- Alignment No. 16483
- gi No. 507209
- % Identity 76.5
- Alignment Length 17
- Location of Alignment in SEQ ID NO 2713: from 5 to 21
- Alignment No. 16484
- gi No. 81638
- % Identity 72.2
- Alignment Length 18
- Location of Alignment in SEQ ID NO 2713: from 5 to 22

- (A) Polynucleotide Sequence
 - Pat. Appln. SEQ ID NO 2714
 - Ceres seq_id 1504333
 - (B) Polypeptide Sequence
 - Pat. Appln. SEQ ID NO 2715
 - Ceres seq_id 1504334
 - Location of start within SEQ ID NO 2714: at 2 nt.
- (C) Nomination and Annotation of Domains within Predicted Polypeptide(s) $% \left(\frac{1}{2}\right) =\frac{1}{2}\left(\frac{1}{2}\right) +\frac{1}{2}\left(\frac{1}{2}\right) +\frac{$
 - (D) Related Amino Acid Sequences
 - Alignment No. 16485
 - gi No. 4469020
 - % Identity 88.9
 - Alignment Length 99
 - Location of Alignment in SEQ ID NO 2715: from 1 to 99
 - Alignment No. 16486
 - gi No. 4680205
 - % Identity 98.8
 - Alignment Length 83
 - Location of Alignment in SEQ ID NO 2715: from 1 to 83
 - (B) Polypeptide Sequence
 - Pat. Appln. SEQ ID NO 2716
 - Ceres seq_id 1504335
 - Location of start within SEQ ID NO 2714: at 20 nt.
- - (D) Related Amino Acid Sequences
 - Alignment No. 16487
 - gi No. 4469020
 - % Identity 88.9
 - Alignment Length 99
 - Location of Alignment in SEQ ID NO 2716: from 1 to 93

- Alignment No. 16488
- gi No. 4680205
- % Identity 98.8
- Alignment Length 83
- Location of Alignment in SEQ ID NO 2716: from 1 to 77
- (B) Polypeptide Sequence
 - Pat. Appln. SEQ ID NO 2717
 - Ceres seq id 1504336
 - Location of start within SEQ ID NO 2714: at 107 nt.
- (C) Nomination and Annotation of Domains within Predicted Polypeptide(s)
 - (D) Related Amino Acid Sequences
 - Alignment No. 16489
 - gi No. 4469020
 - % Identity 88.9
 - Alignment Length 99
 - Location of Alignment in SEQ ID NO 2717: from 1 to 64
 - Alignment No. 16490
 - gi No. 4680205
 - % Identity 98.8
 - Alignment Length 83
 - Location of Alignment in SEQ ID NO 2717: from 1 to 48

- (A) Polynucleotide Sequence
 - Pat. Appln. SEQ ID NO 2718
 - Ceres seq_id 1504370
 - (B) Polypeptide Sequence
 - Pat. Appln. SEQ ID NO 2719
 - Ceres seq_id 1504371
 - Location of start within SEQ ID NO 2718: at 1 nt.
- - (D) Related Amino Acid Sequences
 - (B) Polypeptide Sequence
 - Pat. Appln. SEQ ID NO 2720
 - Ceres seq_id 1504372
 - Location of start within SEQ ID NO 2718: at 2 nt.
- (C) Nomination and Annotation of Domains within Predicted Polypeptide(s) $\label{eq:condition}$
 - (D) Related Amino Acid Sequences
 - Alignment No. 16491
 - gi No. 2997589
 - % Identity 87.1
 - Alignment Length 116
 - Location of Alignment in SEQ ID NO 2720: from 1 to 116
 - Alignment No. 16492
 - gi No. 2997591
 - % Identity 84.6
 - Alignment Length 117
 - Location of Alignment in SEQ ID NO 2720: from 1 to 117
 - Alignment No. 16493

- gi No. 2997593
- % Identity 86.3
- Alignment Length 117
- Location of Alignment in SEQ ID NO 2720: from 1 to 117
- Alignment No. 16494
- gi No. 3319374
- % Identity 79.2
- Alignment Length 24
- Location of Alignment in SEQ ID NO 2720: from 93 to 116
- Alignment No. 16495
- gi No. 3367515
- % Identity 82.9
- Alignment Length 117
- Location of Alignment in SEQ ID NO 2720: from 1 to 117
- (B) Polypeptide Sequence
 - Pat. Appln. SEQ ID NO 2721
 - Ceres seq_id 1504373
 - Location of start within SEQ ID NO 2718: at 23 nt.
- - (D) Related Amino Acid Sequences
 - Alignment No. 16496
 - gi No. 2997589
 - % Identity 87.1
 - Alignment Length 116
 - Location of Alignment in SEQ ID NO 2721: from 1 to 109
 - Alignment No. 16497
 - gi No. 2997591
 - % Identity 84.6
 - Alignment Length 117
 - Location of Alignment in SEQ ID NO 2721: from 1 to 110 $\,$
 - Alignment No. 16498
 - gi No. 2997593
 - % Identity 86.3
 - Alignment Length 117
 - Location of Alignment in SEQ ID NO 2721: from 1 to 110
 - Alignment No. 16499
 - gi No. 3319374
 - % Identity 79.2
 - Alignment Length 24
 - Location of Alignment in SEQ ID NO 2721: from 86 to 109
 - Alignment No. 16500
 - gi No. 3367515
 - % Identity 82.9
 - Alignment Length 117
 - Location of Alignment in SEQ ID NO 2721: from 1 to 110

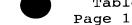
- (A) Polynucleotide Sequence
 - Pat. Appln. SEQ ID NO 2722
 - Ceres seq_id 1504374
 - (B) Polypeptide Sequence
 - Pat. Appln. SEQ ID NO 2723

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- Ceres seq_id 1504375
- Location of start within SEQ ID NO 2722: at 3 nt.
- (C) Nomination and Annotation of Domains within Predicted Polypeptide(s) $% \left(1\right) =\left(1\right) \left(1\right) +\left(1\right) \left(1\right) \left(1\right) +\left(1\right) \left(1\right)$
 - Alignment No. 16501
 - E1-E2 ATPases
 - Location within SEQ ID NO 2723: from 2 to 149 aa.
 - (D) Related Amino Acid Sequences
 - Alignment No. 16502
 - gi No. 2668492
 - % Identity 77.7
 - Alignment Length 148
 - Location of Alignment in SEQ ID NO 2723: from 2 to 149
 - Alignment No. 16503
 - gi No. 3549654
 - % Identity 77.7
 - Alignment Length 148
 - Location of Alignment in SEQ ID NO 2723: from 2 to 149
 - Alignment No. 16504
 - gi No. 4490319
 - % Identity 77.7
 - Alignment Length 148
 - Location of Alignment in SEQ ID NO 2723: from 2 to 149
 - (B) Polypeptide Sequence
 - Pat. Appln. SEQ ID NO 2724
 - Ceres seq id 1504376
 - Location of start within SEQ ID NO 2722: at 12 nt.
- (C) Nomination and Annotation of Domains within Predicted Polypeptide(s)
 - Alignment No. 16505
 - E1-E2 ATPases
 - Location within SEQ ID NO 2724: from 1 to 146 aa.
 - (D) Related Amino Acid Sequences
 - Alignment No. 16506
 - gi No. 2668492
 - % Identity 77.7
 - Alignment Length 148
 - Location of Alignment in SEQ ID NO 2724: from 1 to 146
 - Alignment No. 16507
 - gi No. 3549654
 - % Identity 77.7
 - Alignment Length 148
 - Location of Alignment in SEQ ID NO 2724: from 1 to 146
 - Alignment No. 16508
 - qi No. 4490319
 - % Identity 77.7
 - Alignment Length 148
 - Location of Alignment in SEQ ID NO 2724: from 1 to 146
 - (B) Polypeptide Sequence
 - Pat. Appln. SEQ ID NO 2725
 - Ceres seq_id 1504377

- Location of start within SEQ ID NO 2722: at 42 nt.
- (C) Nomination and Annotation of Domains within Predicted Polypeptide(s)
 - Alignment No. 16509
 - E1-E2 ATPases
 - Location within SEQ ID NO 2725: from 1 to 136 aa.
 - (D) Related Amino Acid Sequences
 - Alignment No. 16510
 - gi No. 2668492
 - % Identity 77.7
 - Alignment Length 148
 - Location of Alignment in SEQ ID NO 2725: from 1 to 136
 - Alignment No. 16511
 - gi No. 3549654
 - % Identity 77.7
 - Alignment Length 148
 - Location of Alignment in SEQ ID NO 2725: from 1 to 136
 - Alignment No. 16512
 - gi No. 4490319
 - % Identity 77.7
 - Alignment Length 148
 - Location of Alignment in SEQ ID NO 2725: from 1 to 136

- (A) Polynucleotide Sequence
 - Pat. Appln. SEQ ID NO 2726
 - Ceres seq id 1504382
 - (B) Polypeptide Sequence
 - Pat. Appln. SEQ ID NO 2727
 - Ceres seq id 1504383
 - Location of start within SEQ ID NO 2726: at 2 nt.
- (C) Nomination and Annotation of Domains within Predicted Polypeptide(s)
 - (D) Related Amino Acid Sequences
 - Alignment No. 16513
 - gi No. 100490
 - % Identity 91.7
 - Alignment Length 12
 - Location of Alignment in SEQ ID NO 2727: from 36 to 47
 - Alignment No. 16514
 - gi No. 100490
 - % Identity 85.7
 - Alignment Length 21
 - Location of Alignment in SEQ ID NO 2727: from 27 to 47
 - Alignment No. 16515
 - gi No. 100490
 - % Identity 85.7
 - Alignment Length 21
 - Location of Alignment in SEQ ID NO 2727: from 27 to 47
 - Alignment No. 16516
 - gi No. 100490
 - % Identity 85.7
 - Alignment Length 21



- Location of Alignment in SEQ ID NO 2727: from 27 to 47 - Alignment No. 16517
- gi No. 100524 - % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 16518
- gi No. 100524
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 16519
- gi No. 100524
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 16520
- gi No. 100524
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 16521
- gi No. 100524
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 16522
- qi No. 100524
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 16523
- gi No. 100525
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 16524
- gi No. 100525
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 16525
- gi No. 100525
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 16526
- gi No. 100525
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47

- Alignment No. 16527

- gi No. 100525
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 16528
- gi No. 100598
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 16529
- gi No. 100599
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 16530
- qi No. 100812
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 16531
- gi No. 100934
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 16532
- gi No. 100934
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 16533
- gi No. 100934
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 16534
- gi No. 100934
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 16535
- qi No. 100934
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 16536
- gi No. 100934
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47

- Alignment No. 16537 - gi No. 100934 - % Identity 85.7 - Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 16538
- gi No. 102062
- % Identity 81
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 16539
- gi No. 102278
- % Identity 86.4
- Alignment Length 22
- Location of Alignment in SEQ ID NO 2727: from 27 to 48
- Alignment No. 16540
- qi No. 102278
- % Identity 86.4
- Alignment Length 22
- Location of Alignment in SEQ ID NO 2727: from 27 to 48
- Alignment No. 16541
- gi No. 102278
- % Identity 86.4
- Alignment Length 22
- Location of Alignment in SEQ ID NO 2727: from 27 to 48
- Alignment No. 16542
- gi No. 102278
- % Identity 86.4
- Alignment Length 22
- Location of Alignment in SEQ ID NO 2727: from 27 to 48
- Alignment No. 16543
- gi No. 102278
- % Identity 86.4
- Alignment Length 22
- Location of Alignment in SEQ ID NO 2727: from 27 to 48
- Alignment No. 16544 gi No. 102278

 - % Identity 86.4
 - Alignment Length 22
 - Location of Alignment in SEQ ID NO 2727: from 27 to 48
 - Alignment No. 16545
 - gi No. 102278
 - % Identity 86.4
 - Alignment Length 22
 - Location of Alignment in SEQ ID NO 2727: from 27 to 48
 - Alignment No. 16546
 - gi No. 102279
 - % Identity 86.4
 - Alignment Length 22
 - Location of Alignment in SEQ ID NO 2727: from 27 to 48
 - Alignment No. 16547

- gi No. 102279 - % Identity 86.4 - Alignment Length 22 - Location of Alignment in SEQ ID NO 2727: from 27 to 48 - Alignment No. 16548 - gi No. 102279 - % Identity 86.4 - Alignment Length 22 - Location of Alignment in SEQ ID NO 2727: from 27 to 48 - Alignment No. 16549 - gi No. 102280 - % Identity 86.4 - Alignment Length 22 - Location of Alignment in SEQ ID NO 2727: from 27 to 48 - Alignment No. 16550 - gi No. 102280 - % Identity 86.4 - Alignment Length 22 - Location of Alignment in SEQ ID NO 2727: from 27 to 48 - Alignment No. 16551 - gi No. 102280 - % Identity 86.4 - Alignment Length 22 - Location of Alignment in SEQ ID NO 2727: from 27 to 48 - Alignment No. 16552 - gi No. 102280 - % Identity 86.4 - Alignment Length 22 - Location of Alignment in SEQ ID NO 2727: from 27 to 48 - Alignment No. 16553 - gi No. 102280 - % Identity 86.4 - Alignment Length 22 - Location of Alignment in SEQ ID NO 2727: from 27 to 48 - Alignment No. 16554 - gi No. 102281 - % Identity 86.4 - Alignment Length 22 - Location of Alignment in SEQ ID NO 2727: from 27 to 48 - Alignment No. 16555
 - Alignment No. 16556
 - gi No. 102281

gi No. 102281% Identity 86.4Alignment Length 22

- % Identity 86.4
- Alignment Length 22
- Location of Alignment in SEQ ID NO 2727: from 27 to 48

- Location of Alignment in SEQ ID NO 2727: from 27 to 48

- Alignment No. 16557
- gi No. 102281

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- % Identity 86.4
- Alignment Length 22
- Location of Alignment in SEQ ID NO 2727: from 27 to 48
- Alignment No. 16558
- gi No. 102281
- % Identity 86.4
- Alignment Length 22
- Location of Alignment in SEQ ID NO 2727: from 27 to 48
- Alignment No. 16559
- gi No. 102389
- % Identity 81
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 16560
- gi No. 103436
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 16561
- gi No. 1044940
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 16562
- gi No. 104829
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 16563
- qi No. 104829
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 16564
- gi No. 104829
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 16565
- gi No. 1050930
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 16566
- gi No. 1050930
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 16567
- gi No. 10673
- % Identity 81

- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 16568
- gi No. 1070590
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 16569
- gi No. 1070590
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 16570
- gi No. 1070590
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 16571
- gi No. 1070591
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 16572
- gi No. 1070591
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 16573
- gi No. 1070591
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 16574
- gi No. 1070591
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 16575
- gi No. 1070591
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 16576
- gi No. 1070591
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 16577
- gi No. 1070591
- % Identity 85.7
- Alignment Length 21

- Location of Alignment in SEQ ID NO 2727: from 27 to 47 - Alignment No. 16578 - gi No. 1070591 - % Identity 85.7 - Alignment Length 21 - Location of Alignment in SEQ ID NO 2727: from 27 to 47 - Alignment No. 16579 - gi No. 1070591 - % Identity 85.7 - Alignment Length 21 - Location of Alignment in SEQ ID NO 2727: from 27 to 47 - Alignment No. 16580 - gi No. 1076678 - % Identity 85.7 - Alignment Length 21 - Location of Alignment in SEQ ID NO 2727: from 27 to 47 - Alignment No. 16581 - gi No. 1076708 - % Identity 85.7 - Alignment Length 21 - Location of Alignment in SEQ ID NO 2727: from 27 to 47 - Alignment No. 16582 - gi No. 1076708 - % Identity 85.7 - Alignment Length 21 - Location of Alignment in SEQ ID NO 2727: from 27 to 47 - Alignment No. 16583 - gi No. 1076708 - % Identity 85.7 - Alignment Length 21 - Location of Alignment in SEQ ID NO 2727: from 27 to 47 - Alignment No. 16584 - gi No. 1076708 - % Identity 85.7 - Alignment Length 21 - Location of Alignment in SEQ ID NO 2727: from 27 to 47 - Alignment No. 16585 - gi No. 1078777 - % Identity 70.4 - Alignment Length 27 - Location of Alignment in SEQ ID NO 2727: from 27 to 51 - Alignment No. 16586 - gi No. 1078813 - % Identity 71.4
- Alignment No. 16587

- Alignment Length 28

- gi No. 1078813
- % Identity 71.4
- Alignment Length 28
- Location of Alignment in SEQ ID NO 2727: from 27 to 52

- Location of Alignment in SEQ ID NO 2727: from 27 to 52

- % Identity 85.7 - Alignment Length 21

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- Alignment No. 16588
- gi No. 1078813
- % Identity 71.4
- Alignment Length 28
- Location of Alignment in SEQ ID NO 2727: from 27 to 52
- Alignment No. 16589
- gi No. 1083758
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 16590
- gi No. 1083758
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 16591
- qi No. 1083758
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 16592
- gi No. 1083758
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 16593
- gi No. 1083758
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 16594
- gi No. 1083758
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 16595
- gi No. 1083758
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 16596
- gi No. 1083758
- % Identity 85.7
- Alignment Length 21
 - Location of Alignment in SEQ ID NO 2727: from 27 to 47
 - Alignment No. 16597
 - gi No. 1083758
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- Location of Alignment in SEQ ID NO 2727: from 27 to 47

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- Alignment No. 16598 - gi No. 1083758 - % Identity 85.7 - Alignment Length 21 - Location of Alignment in SEQ ID NO 2727: from 27 to 47 - Alignment No. 16599 - gi No. 1101011 - % Identity 76.2 - Alignment Length 21 - Location of Alignment in SEQ ID NO 2727: from 27 to 47 - Alignment No. 16600 - gi No. 1101011 - % Identity 76.2 - Alignment Length 21 - Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 16601 - gi No. 1101011 - % Identity 76.2 - Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 16602 - qi No. 1101011 - % Identity 76.2 - Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 16603 - gi No. 1101011 - % Identity 76.2
- Alignment Length 21 - Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 16604 - gi No. 1101011 - % Identity 76.2 - Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 16605 - gi No. 1101011 - % Identity 76.2 - Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 16606 - gi No. 1101011 - % Identity 76.2 - Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 16607 - gi No. 1101011
- % Identity 76.2
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 16608

- gi No. 1101011% Identity 76.2Alignment Length 21Location of Alignment
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 16609
- gi No. 1101013
- % Identity 73.3
- Alignment Length 15
- Location of Alignment in SEQ ID NO 2727: from 33 to 47
- Alignment No. 16610
- gi No. 1101015
- % Identity 73.3
- Alignment Length 15
- Location of Alignment in SEQ ID NO 2727: from 33 to 47
- Alignment No. 16611
- gi No. 1101021
- % Identity 73.3
- Alignment Length 15
- Location of Alignment in SEQ ID NO 2727: from 33 to 47
- Alignment No. 16612
- gi No. 1101021
- % Identity 76.2
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 16613
- gi No. 1107481
- % Identity 85
- Alignment Length 20
- Location of Alignment in SEQ ID NO 2727: from 27 to 46
- Alignment No. 16614
- gi No. 1107481
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 16615
- gi No. 1107481
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 16616
- gi No. 1143188
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 16617
- gi No. 1143188
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 16618
- gi No. 1143188

- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 16619
- gi No. 1167510
- % Identity 80
- Alignment Length 20
- Location of Alignment in SEQ ID NO 2727: from 27 to 46
- Alignment No. 16620
- gi No. 1167510
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 16621
- gi No. 1174859
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 16622
- gi No. 1174860
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 16623
- gi No. 1174861
- % Identity 81
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 16624
- gi No. 1184755
- % Identity 81
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 16625
- gi No. 1197093
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 16626
- gi No. 1197093
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 16627
- gi No. 1197093
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 16628
- gi No. 1197093
- % Identity 85.7

- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 16629
- gi No. 1304128
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 16630
- gi No. 1304128
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 16631
- gi No. 1304128
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 16632
- gi No. 1304128
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 16633
- gi No. 1304128
- % Identity 81
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 16634
- gi No. 1304128
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 16635
- gi No. 1304128
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 16636
- gi No. 1304128
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 16637
- gi No. 1304357
- % Identity 71.4
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 16638
- gi No. 1321735
- % Identity 85.7
- Alignment Length 21



- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 16639
- qi No. 1321735
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 16640
- gi No. 1326022
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 16641
- gi No. 1326022
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 16642
- qi No. 1332579
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 16643
- gi No. 1332579
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 16644
- gi No. 1332579
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 16645
- gi No. 1332579
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 16646
- gi No. 1332579
- % Identity 81
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 16647
- gi No. 1332579
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 16648
- gi No. 1332579
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47

- Alignment No. 16649 - gi No. 1332579 - % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 16650
- qi No. 1332579
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 16651
- gi No. 1332579
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 16652
- gi No. 1351348
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 16653
- gi No. 1351349
- % Identity 76.2
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 16654
- gi No. 1353755
- % Identity 81
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 16655
- gi No. 1353757
- % Identity 80
- Alignment Length 20
- Location of Alignment in SEQ ID NO 2727: from 28 to 47
- Alignment No. 16656
- gi No. 1353757
- % Identity 81
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 16657
- gi No. 1362008
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 16658
- gi No. 1362008
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47

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- Alignment No. 16659
- gi No. 1362008
- % Identity 71.4
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 16660
- gi No. 1362008
- % Identity 76.2
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 16661
- gi No. 1362009
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 16662
- gi No. 1362010
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 16663
- gi No. 1362010
- % Identity 81
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 16664
- gi No. 1362010
- % Identity 71.4
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 16665
- gi No. 1362012
- % Identity 76.2
- Alignment Length 21
 - Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 16666
 - gi No. 1362012
 - % Identity 76.2
 - Alignment Length 21
 - Location of Alignment in SEQ ID NO 2727: from 27 to 47
 - Alignment No. 16667
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- gi No. 136665
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 16668
- gi No. 136666
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 16669

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- gi No. 136667 - % Identity 85.7 - Alignment Length 21 - Location of Alignme
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 16670
- gi No. 136668
- % Identity 86.4
- Alignment Length 22
- Location of Alignment in SEQ ID NO 2727: from 27 to 48
- Alignment No. 16671
- gi No. 136669
- % Identity 71.4
- Alignment Length 28
- Location of Alignment in SEQ ID NO 2727: from 27 to 52
- Alignment No. 16672
- gi No. 136670
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 16673
- gi No. 136671
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 16674
- gi No. 136672
- % Identity 81
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 16675
- gi No. 136673
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 16676
- gi No. 136674
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 16677
- gi No. 136675
- % Identity 81
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 16678
- gi No. 136676
- % Identity 81
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 16679
- qi No. 136677

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- % Identity 81
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 16680
- gi No. 136678
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 16681
- gi No. 1421797
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 16682
- gi No. 156480
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 16683
- gi No. 158759
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 16684
- gi No. 158763
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 16685
- gi No. 158765
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 16686
- gi No. 158767
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 16687
- gi No. 158769
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 16688
- gi No. 158771
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 16689
- qi No. 161281
- % Identity 85.7

- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 16690
- gi No. 163575
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 16691
- gi No. 163575
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 16692
- gi No. 166336
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 16693
- gi No. 166336
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 16694
- gi No. 166336
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 16695
- gi No. 166336
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 16696
- gi No. 166336
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 16697
- gi No. 166336
- % Identity 81
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 16698
- gi No. 1666175
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 16699
- gi No. 1675359
- % Identity 81
- Alignment Length 21

- Location of Alignment in SEQ ID NO 2727: from 27 to 47 - Alignment No. 16700 - gi No. 167935 - % Identity 86.4 - Alignment Length 22 - Location of Alignment in SEQ ID NO 2727: from 27 to 48 - Alignment No. 16701 - gi No. 167935 - % Identity 86.4 - Alignment Length 22 - Location of Alignment in SEQ ID NO 2727: from 27 to 48 - Alignment No. 16702 - gi No. 167935 - % Identity 86.4 - Alignment Length 22 - Location of Alignment in SEQ ID NO 2727: from 27 to 48 - Alignment No. 16703 - gi No. 167935 - % Identity 86.4 - Alignment Length 22 - Location of Alignment in SEQ ID NO 2727: from 27 to 48 - Alignment No. 16704 - gi No. 167935 - % Identity 86.4 - Alignment Length 22 - Location of Alignment in SEQ ID NO 2727: from 27 to 48 - Alignment No. 16705 - gi No. 167941 - % Identity 81 - Alignment Length 21 - Location of Alignment in SEQ ID NO 2727: from 28 to 48 - Alignment No. 16706 - gi No. 167945 - % Identity 86.4 - Alignment Length 22 - Location of Alignment in SEQ ID NO 2727: from 27 to 48 - Alignment No. 16707 - gi No. 167945 - % Identity 81.8 - Alignment Length 22 - Location of Alignment in SEQ ID NO 2727: from 27 to 48 - Alignment No. 16708 - gi No. 167945 - % Identity 86.4 - Alignment Length 22 - Location of Alignment in SEQ ID NO 2727: from 27 to 48
- Alignment No. 16709
- gi No. 167947
- % Identity 86.4
- Alignment Length 22
- Location of Alignment in SEQ ID NO 2727: from 27 to 48

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- Alignment No. 16710
- gi No. 167947
- % Identity 86.4
- Alignment Length 22
- Location of Alignment in SEQ ID NO 2727: from 27 to 48
- Alignment No. 16711
- gi No. 167947
- % Identity 86.4
- Alignment Length 22
- Location of Alignment in SEQ ID NO 2727: from 27 to 48
- Alignment No. 16712
- gi No. 167947
- % Identity 86.4
- Alignment Length 22
- Location of Alignment in SEQ ID NO 2727: from 27 to 48
- Alignment No. 16713
- gi No. 167947
- % Identity 86.4
- Alignment Length 22
- Location of Alignment in SEQ ID NO 2727: from 27 to 48
- Alignment No. 16714
- gi No. 167947
- % Identity 86.4
- Alignment Length 22
- Location of Alignment in SEQ ID NO 2727: from 27 to 48
- Alignment No. 16715
- gi No. 167947
- % Identity 86.4
- Alignment Length 22
- Location of Alignment in SEQ ID NO 2727: from 27 to 48
- Alignment No. 16716
- gi No. 167949
- % Identity 86.4
- Alignment Length 22
- Location of Alignment in SEQ ID NO 2727: from 27 to 48
- Alignment No. 16717
- gi No. 167949
- % Identity 86.4
- Alignment Length 22
- Location of Alignment in SEQ ID NO 2727: from 27 to 48
- Alignment No. 16718
- gi No. 167949
- % Identity 86.4
- Alignment Length 22
- Location of Alignment in SEQ ID NO 2727: from 27 to 48
- Alignment No. 16719
- gi No. 167949
- % Identity 86.4
- Alignment Length 22
- Location of Alignment in SEQ ID NO 2727: from 27 to 48
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- Alignment No. 16720 - qi No. 167949 - % Identity 86.4 - Alignment Length 22 - Location of Alignment in SEQ ID NO 2727: from 27 to 48 - Alignment No. 16721 - gi No. 1684855 - % Identity 85.7 - Alignment Length 21 - Location of Alignment in SEQ ID NO 2727: from 27 to 47 - Alignment No. 16722 - gi No. 1684855 - % Identity 85.7 - Alignment Length 21 - Location of Alignment in SEQ ID NO 2727: from 27 to 47 - Alignment No. 16723 - gi No. 1684855 - % Identity 85.7 - Alignment Length 21 - Location of Alignment in SEQ ID NO 2727: from 27 to 47 - Alignment No. 16724 - gi No. 1684855
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 16725
- gi No. 1684857
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 16726
- qi No. 1684857
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 16727
- gi No. 170352
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 16728
- gi No. 170352
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 16729
- gi No. 170352
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 16730

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- gi No. 170352
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 16731
- gi No. 170352
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 16732
- gi No. 170352
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 16733
- gi No. 170354
- % Identity 88.2
- Alignment Length 17
- Location of Alignment in SEQ ID NO 2727: from 31 to 47
- Alignment No. 16734
- gi No. 170354
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 16735
- gi No. 170354
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 16736
- gi No. 170354
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 16737
- gi No. 170354
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 16738
- gi No. 1762374
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 16739
- gi No. 1762935
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 16740
- gi No. 1763015

- % Identity 85.7

- Alignment Length 21

- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 16741
- gi No. 1771780
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 16742
- gi No. 1778712
- % Identity 81
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 16743
- gi No. 1778712
- % Identity 81
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 16744
- gi No. 1778712
- % Identity 81
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 16745
- gi No. 1778712
- % Identity 81
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 16746
- gi No. 1778712
- % Identity 81
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 16747
- gi No. 1800281
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 16748
- gi No. 1800281
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 16749
- qi No. 1800281
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 16750
- gi No. 1800281
- % Identity 85.7

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- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 16751
- gi No. 1800281
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 16752
- gi No. 1805696
- % Identity 85.7
- Alignment Length 14
- Location of Alignment in SEQ ID NO 2727: from 34 to 47
- Alignment No. 16753
- qi No. 1805696
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 16754
- gi No. 1839584
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 16755
- gi No. 1841849
- % Identity 87.5
- Alignment Length 16
- Location of Alignment in SEQ ID NO 2727: from 27 to 42
- Alignment No. 16756
- gi No. 208558
- % Identity 81
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 16757
- gi No. 208560
- % Identity 81
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 16758
- gi No. 208562
- % Identity 76.2
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 16759
- gi No. 208564
- % Identity 76.2
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 16760
- gi No. 208566
- % Identity 81
- Alignment Length 21

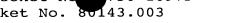
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 - Alignment No. 16761
 - gi No. 208568
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 - Alignment Length 21
 - Location of Alignment in SEQ ID NO 2727: from 27 to 47
 - Alignment No. 16762
 - gi No. 208891
 - % Identity 80
 - Alignment Length 20
 - Location of Alignment in SEQ ID NO 2727: from 27 to 46
 - Alignment No. 16763
 - gi No. 208891
 - % Identity 85.7
 - Alignment Length 21
 - Location of Alignment in SEQ ID NO 2727: from 27 to 47
 - Alignment No. 16764
 - gi No. 209603
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 - Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 16765
- gi No. 2118958
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 16766
- gi No. 2118958
- % Identity 85.7
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- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 16767
- gi No. 2118958
- % Identity 85.7
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- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 16768
- gi No. 2118958
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 16769
- gi No. 2118958
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 16770
- gi No. 2118959
- % Identity 81.8
- Alignment Length 22
- Location of Alignment in SEQ ID NO 2727: from 27 to 48
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- Alignment No. 16771 - gi No. 2118959
- % Identity 77.3
- Alignment Length 22
- Location of Alignment in SEQ ID NO 2727: from 27 to 48
- Alignment No. 16772
- gi No. 2118959
- % Identity 72.7
- Alignment Length 22
- Location of Alignment in SEQ ID NO 2727: from 27 to 48
- Alignment No. 16773
- gi No. 2118960
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 16774
- gi No. 2118960
- % Identity 85.7
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- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 16775
- gi No. 2118961
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 16776
- gi No. 2118961
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 16777
- gi No. 2118962
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 16778
- gi No. 2118962
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 16779
- gi No. 2118964
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 16780
- gi No. 2118964
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47

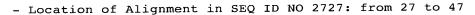
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- Alignment No. 16782
- gi No. 2118965
- % Identity 85.7
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- Alignment No. 16783
- gi No. 2118965
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- Alignment No. 16784
- gi No. 2118965
- % Identity 85.7
- Alignment Length 21
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- Alignment No. 16785
- gi No. 2129452
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 16786
- gi No. 2129452
- % Identity 81
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 16787
- gi No. 2129452
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 16788
- gi No. 2129452
- % Identity 85.7
- Alignment Length 21
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- Alignment No. 16789
- gi No. 2129452
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 16790
- gi No. 2129452
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 16791

- gi No. 2133278
- % Identity 75
- Alignment Length 28
- Location of Alignment in SEQ ID NO 2727: from 27 to 52
- Alignment No. 16792
- gi No. 2133549
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 16793
- gi No. 2144011
- % Identity 85.7
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- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 16794
- qi No. 2144275
- % Identity 85.7
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- Alignment No. 16795
- gi No. 2144734
- % Identity 81
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 16796
- gi No. 2144734
- % Identity 81
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 16797
- gi No. 2144734
- % Identity 81
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 16798
- gi No. 2144734
- % Identity 81
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 16799
- gi No. 2149467
- % Identity 85.7
- Alignment Length 21
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- Alignment No. 16800
- gi No. 2209091
- % Identity 81
- Alignment Length 21
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- Alignment No. 16801
- gi No. 2209091

- % Identity 81
- Alignment Length 21
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- Alignment No. 16802
- gi No. 223061
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 16803
- gi No. 224321
- % Identity 85.7
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- Alignment No. 16804
- gi No. 224321
- % Identity 85.7
- Alignment Length 21
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- Alignment No. 16805
- gi No. 225317
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 16806
- gi No. 225319
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 16807
- gi No. 225320
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 16808
- gi No. 2281952
- % Identity 85.7
- Alignment Length 14
- Location of Alignment in SEQ ID NO 2727: from 34 to 47
- Alignment No. 16809
- gi No. 2281954
- % Identity 85.7
- Alignment Length 14
- Location of Alignment in SEQ ID NO 2727: from 34 to 47
- Alignment No. 16810
- gi No. 2281955
- % Identity 85.7
- Alignment Length 14
- Location of Alignment in SEQ ID NO 2727: from 34 to 47
- Alignment No. 16811
- gi No. 2281959
- % Identity 73.3



- Alignment Length 15
- Location of Alignment in SEQ ID NO 2727: from 33 to 47
- Alignment No. 16812
- gi No. 2330875
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 16813
- gi No. 2408009
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 16814
- qi No. 2437825
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 16815
- gi No. 2437825
- % Identity 85.7
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- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 16816
- gi No. 2437825
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 16817
- gi No. 2437825
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 16818
- gi No. 247308
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 16819
- gi No. 248865
- % Identity 80
- Alignment Length 20
- Location of Alignment in SEQ ID NO 2727: from 27 to 46
- Alignment No. 16820
- gi No. 2558539
- % Identity 81
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 16821
- gi No. 2627129
- % Identity 85.7
- Alignment Length 21



- Alignment No. 16822
- gi No. 2627129
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 16823
- gi No. 2627129
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 16824
- gi No. 2627129
- % Identity 85.7
- Alignment Length 21
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- Alignment No. 16825
- gi No. 2627129
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 16826
- gi No. 2627129
- % Identity 81
- Alignment Length 21
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- Alignment No. 16827
- gi No. 2627129
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 16828
- gi No. 2627129
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 16829
- gi No. 2627131
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 16830
- gi No. 2627131
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 16831
- gi No. 2627131
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47

- Alignment Length 21

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- Alignment No. 16832
- gi No. 2627131
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 16833
- gi No. 2627131
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 16834
- gi No. 2627131
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 16835
- gi No. 2627131
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 16836
- gi No. 2627131
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 16837
- qi No. 2627131
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 16838
- gi No. 2627131
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 16839
- gi No. 2627131
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 16840
- gi No. 2627133
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 16841
- gi No. 2627133
- % Identity 85.7
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- Location of Alignment in SEQ ID NO 2727: from 27 to 47

- Alignment No. 16842 - gi No. 2627133 - % Identity 85.7 - Alignment Length 21 - Location of Alignment in SEQ ID NO 2727: from 27 to 47 - Alignment No. 16843 - gi No. 2627133 - % Identity 85.7 - Alignment Length 21 - Location of Alignment in SEQ ID NO 2727: from 27 to 47 - Alignment No. 16844 - gi No. 2627133 - % Identity 85.7 - Alignment Length 21 - Location of Alignment in SEQ ID NO 2727: from 27 to 47 - Alignment No. 16845 - gi No. 2627133 - % Identity 85.7 - Alignment Length 21 - Location of Alignment in SEQ ID NO 2727: from 27 to 47 - Alignment No. 16846 - qi No. 2627133 - % Identity 85.7 - Alignment Length 21 - Location of Alignment in SEQ ID NO 2727: from 27 to 47 - Alignment No. 16847 - gi No. 2627133 - % Identity 85.7 - Alignment Length 21 - Location of Alignment in SEQ ID NO 2727: from 27 to 47 - Alignment No. 16848 - gi No. 2627133 - % Identity 85.7 - Alignment Length 21 - Location of Alignment in SEQ ID NO 2727: from 27 to 47 - Alignment No. 16849 - gi No. 2627133 - % Identity 85.7 - Alignment Length 21 - Location of Alignment in SEQ ID NO 2727: from 27 to 47 - Alignment No. 16850 - gi No. 2627133
- Alignment No. 16851
- gi No. 2627133
- % Identity 85.7

- % Identity 85.7- Alignment Length 21

- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47

- Location of Alignment in SEQ ID NO 2727: from 27 to 47

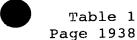
- Alignment No. 16852

- gi No. 2627133
 % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 16853
- qi No. 2641213
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 16854
- gi No. 2641213
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 16855
- gi No. 2654141
- % Identity 81
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 16856
- gi No. 2654141
- % Identity 76.2
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 16857
- gi No. 2654141
- % Identity 81
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47 $\,$
- Alignment No. 16858
- gi No. 2654141
- % Identity 81
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 16859
- gi No. 2654141
- % Identity 81
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 16860
- gi No. 2707837
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 16861
- gi No. 2707837
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 16862
- gi No. 2707837

- Alignment No. 16872 - gi No. 2760347 - % Identity 85.7

- % Identity 85.7 - Alignment Length 21 - Location of Alignment in SEQ ID NO 2727: from 27 to 47 - Alignment No. 16863 - gi No. 2707837 - % Identity 85.7 - Alignment Length 21 - Location of Alignment in SEQ ID NO 2727: from 27 to 47 - Alignment No. 16864 - gi No. 2739333 - % Identity 85.7 - Alignment Length 21 - Location of Alignment in SEQ ID NO 2727: from 27 to 47 - Alignment No. 16865 - gi No. 2739333 - % Identity 85.7 - Alignment Length 21 - Location of Alignment in SEQ ID NO 2727: from 27 to 47 - Alignment No. 16866 - gi No. 2739333 - % Identity 85.7 - Alignment Length 21 - Location of Alignment in SEQ ID NO 2727: from 27 to 47 - Alignment No. 16867 - gi No. 2739333 - % Identity 85.7 - Alignment Length 21 - Location of Alignment in SEQ ID NO 2727: from 27 to 47 - Alignment No. 16868 - gi No. 2760345 - % Identity 85.7 - Alignment Length 21 - Location of Alignment in SEQ ID NO 2727: from 27 to 47 - Alignment No. 16869 - gi No. 2760345 - % Identity 85.7 - Alignment Length 21 - Location of Alignment in SEQ ID NO 2727: from 27 to 47 - Alignment No. 16870 - gi No. 2760345 - % Identity 85.7 - Alignment Length 21 - Location of Alignment in SEQ ID NO 2727: from 27 to 47 - Alignment No. 16871 - gi No. 2760345 - % Identity 85.7 - Alignment Length 21 - Location of Alignment in SEQ ID NO 2727: from 27 to 47

- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 16873
- gi No. 2760347
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 16874
- gi No. 2760347
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 16875
- gi No. 2760347
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 16876
- gi No. 2760347
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 16877
- gi No. 2760347
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 16878
- gi No. 2760349
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 16879
- gi No. 2760349
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 16880
- gi No. 2760349
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 16881
- gi No. 2760349
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 16882
- gi No. 2760349
- % Identity 85.7
- Alignment Length 21



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- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 16883
- gi No. 279635
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 16884
- gi No. 279636
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 16885
- gi No. 280386
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 16886
- gi No. 281276
- % Identity 80
- Alignment Length 20
- Location of Alignment in SEQ ID NO 2727: from 27 to 46
- Alignment No. 16887
- gi No. 283496
- % Identity 81
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 16888
- gi No. 283496
- % Identity 81
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 16889
- gi No. 283496
- % Identity 81
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 16890
- gi No. 283496
- % Identity 81
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 16891
 - gi No. 283496
- % Identity 81
 - Alignment Length 21
 - Location of Alignment in SEQ ID NO 2727: from 27 to 47
 - Alignment No. 16892
 - gi No. 2894304
 - % Identity 85.7
 - Alignment Length 21
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- Location of Alignment in SEQ ID NO 2727: from 27 to 47

- Alignment No. 16893

- gi No. 2894304
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 16894
- gi No. 2894304
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 16895
- qi No. 2894304
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 16896
- gi No. 2894306
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 16897
- gi No. 2894308
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 16898
- gi No. 2894308
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 16899
- gi No. 2894308
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 16900
- gi No. 2894308
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 16901
- gi No. 2894308
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 16902
- gi No. 2995949
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47

- Alignment No. 16903 - gi No. 3047314 - % Identity 85.7 - Alignment Length 21 - Location of Alignment in SEQ ID NO 2727: from 27 to 47 - Alignment No. 16904 - gi No. 3047316 - % Identity 85.7 - Alignment Length 21 - Location of Alignment in SEQ ID NO 2727: from 27 to 47 - Alignment No. 16905 - gi No. 3047318 - % Identity 85.7 - Alignment Length 21 - Location of Alignment in SEQ ID NO 2727: from 27 to 47 - Alignment No. 16906 - gi No. 3047318 - % Identity 85.7 - Alignment Length 21 - Location of Alignment in SEQ ID NO 2727: from 27 to 47 - Alignment No. 16907 - gi No. 3047318 - % Identity 85.7 - Alignment Length 21 - Location of Alignment in SEQ ID NO 2727: from 27 to 47 - Alignment No. 16908 - gi No. 3047318 - % Identity 85.7 - Alignment Length 21 - Location of Alignment in SEQ ID NO 2727: from 27 to 47 - Alignment No. 16909 - gi No. 3047318 - % Identity 85.7 - Alignment Length 21 - Location of Alignment in SEQ ID NO 2727: from 27 to 47 - Alignment No. 16910 - gi No. 3091264 - % Identity 85.7 - Alignment Length 21 - Location of Alignment in SEQ ID NO 2727: from 27 to 47 - Alignment No. 16911
 - Alignment No. 16912
 - gi No. 3091264

gi No. 3091264% Identity 85.7Alignment Length 21

- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47

- Location of Alignment in SEQ ID NO 2727: from 27 to 47

- Alignment No. 16913

- gi No. 320608

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- gi No. 3091264
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 16914
- gi No. 3126967
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 16915
- gi No. 3126967
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 16916
- gi No. 3126967
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 16917
- gi No. 3126967
- % Identity 81
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 16918
- gi No. 3126967
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 16919
- gi No. 3126967
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 16920
- gi No. 3152950
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 16921
- gi No. 3158372
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 16922
- gi No. 3158372
- % Identity 81
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 16923
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- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 16924
- gi No. 320608
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 16925
- gi No. 320608
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 16926
- gi No. 320608
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 16927
- gi No. 322750
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 16928
- gi No. 323071
- % Identity 76.2
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 16929
- gi No. 323157
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 16930
- gi No. 323157
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 16931
- gi No. 323157
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 16932
- gi No. 323157
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 16933
- gi No. 323157
- % Identity 85.7

- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 16934
- gi No. 323157
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 16935
- gi No. 323208
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 16936
- gi No. 323230
- % Identity 81
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 16937
- gi No. 3265058
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 16938
- gi No. 3319208
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 16939
- gi No. 3335355
- % Identity 85
- Alignment Length 20
- Location of Alignment in SEQ ID NO 2727: from 27 to 46
- Alignment No. 16940
- gi No. 3335355
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 16941
- gi No. 3335355
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 16942
- gi No. 3335355
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 16943
- gi No. 340062
- % Identity 88.2
- Alignment Length 17

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- Location of Alignment in SEQ ID NO 2727: from 31 to 47 Alignment No. 16944
- gi No. 3452083
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 16945
- gi No. 348148
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 16946
- gi No. 3603456
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 16947
- gi No. 3603456
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 16948
- gi No. 3603456
- % Identity 75
- Alignment Length 28
- Location of Alignment in SEQ ID NO 2727: from 27 to 52
- Alignment No. 16949
- gi No. 3687425
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 16950
- gi No. 3687425
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 16951
- gi No. 3687425
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 16952
- gi No. 3738185
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 16953
- gi No. 3738185
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47

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- Alignment No. 16954
- gi No. 3738185
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 16955
- gi No. 3738185
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 16956
- gi No. 3738185
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 16957
- gi No. 3776536
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 16958
- gi No. 3776536
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 16959
- gi No. 3776536
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 16960
- gi No. 3776536
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 16961
- gi No. 3776536
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 16962
- gi No. 3776536
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 16963
- gi No. 3776536
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
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- Alignment No. 16964 - gi No. 3776536 - % Identity 85.7 - Alignment Length 21 - Location of Alignment in SEQ ID NO 2727: from 27 to 47 - Alignment No. 16965 - gi No. 3789940 - % Identity 85.7 - Alignment Length 21 - Location of Alignment in SEQ ID NO 2727: from 27 to 47 - Alignment No. 16966 - gi No. 3789940 - % Identity 85.7 - Alignment Length 21 - Location of Alignment in SEQ ID NO 2727: from 27 to 47 - Alignment No. 16967 - gi No. 3789940 - % Identity 81 - Alignment Length 21 - Location of Alignment in SEQ ID NO 2727: from 27 to 47 - Alignment No. 16968 - gi No. 3789940 - % Identity 85.7 - Alignment Length 21 - Location of Alignment in SEQ ID NO 2727: from 27 to 47 - Alignment No. 16969 - gi No. 3789942 - % Identity 85.7 - Alignment Length 21 - Location of Alignment in SEQ ID NO 2727: from 27 to 47 - Alignment No. 16970 - gi No. 3789942 - % Identity 85.7 - Alignment Length 21 - Location of Alignment in SEQ ID NO 2727: from 27 to 47 - Alignment No. 16971 - gi No. 3789942 - % Identity 85.7 - Alignment Length 21 - Location of Alignment in SEQ ID NO 2727: from 27 to 47 - Alignment No. 16972 - gi No. 3789942 - % Identity 85.7 - Alignment Length 21 - Location of Alignment in SEQ ID NO 2727: from 27 to 47

- Location of Alignment in SEQ ID NO 2727: from 27 to 47

- Alignment No. 16974

Alignment No. 16973gi No. 3789942% Identity 85.7Alignment Length 21

- gi No. 385076
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 16975
- gi No. 3882081
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 16976
- gi No. 3882081
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 16977
- gi No. 3882081
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 16978
- gi No. 3885463
- % Identity 83.3
- Alignment Length 18
- Location of Alignment in SEQ ID NO 2727: from 30 to 47
- Alignment No. 16979
- gi No. 3892189
- % Identity 70.4
- Alignment Length 27
- Location of Alignment in SEQ ID NO 2727: from 27 to 51
- Alignment No. 16980
- gi No. 402242
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 16981
- gi No. 4105408
- % Identity 91.7
- Alignment Length 12
- Location of Alignment in SEQ ID NO 2727: from 36 to 47
- Alignment No. 16982
- gi No. 4105408
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 16983
- gi No. 4105408
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 16984
- gi No. 4105408

- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 16985
- gi No. 4115337
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 16986
- gi No. 4115337
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 16987
- gi No. 4115337
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 16988
- gi No. 4115337
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 16989
- gi No. 4115337
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 16990
- gi No. 4115337
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 16991
- gi No. 4150898
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 16992
- qi No. 4150898
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 16993
- gi No. 4150898
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 16994
- gi No. 4150898
- % Identity 85.7

- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 16995
- gi No. 4150912
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 16996
- gi No. 4150912
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 16997
- gi No. 4150912
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 16998
- gi No. 4150912
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 16999
- gi No. 4150912
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 17000
- gi No. 4150914
- % Identity 86.7
- Alignment Length 15
- Location of Alignment in SEQ ID NO 2727: from 33 to 47
- Alignment No. 17001
- gi No. 4150914
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 17002
- gi No. 4151082
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 17003
- gi No. 418854
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 17004
- gi No. 418854
- % Identity 85.7
- Alignment Length 21

- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 17005
- gi No. 418854
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 17006
- gi No. 418854
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 17007
- gi No. 418854
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 17008
- gi No. 418854
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 17009
- gi No. 421735
- % Identity 88.9
- Alignment Length 18
- Location of Alignment in SEQ ID NO 2727: from 27 to 44
- Alignment No. 17010
- gi No. 421867
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 17011
- qi No. 421929
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 17012
- gi No. 421929
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 17013
- gi No. 421929
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 17014
- gi No. 421929
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47

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- Alignment No. 17015
- gi No. 421929
- % Identity 81
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 17016
- gi No. 421929
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 17017
- gi No. 421929
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 17018
- gi No. 422248
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 17019
- gi No. 422248
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 17020
- gi No. 422248
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 17021
- gi No. 422248
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 17022
- gi No. 422248
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 17023
- gi No. 422269
- % Identity 81
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 17024
- gi No. 422270
- % Identity 76.2
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
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- Alignment No. 17025
- gi No. 422271
- % Identity 81
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 17026
- gi No. 433970
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 17027
- gi No. 433970
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 17028
- gi No. 433970
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 17029
- gi No. 433970
- % Identity 81
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 17030
- gi No. 433970
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 17031
- gi No. 444791
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 17032
- gi No. 444791
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 17033
- gi No. 444791
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 17034
- gi No. 444791
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 17035

- gi No. 4506713
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 17036
- gi No. 4507761
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 17037
- gi No. 456779
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 17038
- gi No. 4586594
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 17039
- gi No. 4586594
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 17040
- gi No. 4587232
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 17041
- gi No. 4587234
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 17042
- gi No. 4587236
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 17043
- gi No. 4587236
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 17044
- gi No. 4587236
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 17045
- gi No. 4587236

- % Identity 85.7

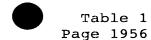
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47

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- Alignment No. 17046
- gi No. 4587236
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 17047
- gi No. 4587236
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 17048
- gi No. 4587236
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 17049
- gi No. 4587236
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 17050
- gi No. 4587236
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 17051
- gi No. 4587236
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 17052
- gi No. 4587236
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 17053
- gi No. 4587236
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 17054
- gi No. 4589760
- % Identity 75
- Alignment Length 28
- Location of Alignment in SEQ ID NO 2727: from 27 to 52
- Alignment No. 17055
- gi No. 4589760
- % Identity 75

- Alignment Length 28
- Location of Alignment in SEQ ID NO 2727: from 27 to 52
- Alignment No. 17056
- gi No. 463363
- % Identity 70
- Alignment Length 20
- Location of Alignment in SEQ ID NO 2727: from 27 to 46
- Alignment No. 17057
- gi No. 463369
- % Identity 71.4
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 17058
- gi No. 463373
- % Identity 76.2
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 17059
- gi No. 463375
- % Identity 76.2
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 17060
- gi No. 464989
- % Identity 71.4
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- Alignment No. 17061
- gi No. 464990
- % Identity 81
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 17062
- gi No. 468272
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 17063
- gi No. 4737
- % Identity 81
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 17064
- gi No. 477630
- % Identity 85.7
- Alignment Length 21
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- Alignment No. 17065
- gi No. 477815
- % Identity 81
- Alignment Length 21



- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 17066
- gi No. 478811
- % Identity 85.7
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- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 17067
- gi No. 478811
- % Identity 85.7
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- Alignment No. 17068
- gi No. 478811
- % Identity 85.7
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- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 17069
- gi No. 478811
- % Identity 85.7
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- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 17070
- gi No. 4809266
- % Identity 85.7
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- Alignment No. 17071
- gi No. 4809266
- % Identity 85.7
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- Alignment No. 17072
- gi No. 4809266
- % Identity 85.7
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- Alignment No. 17073
- gi No. 4809266
- % Identity 85.7
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- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 17074
- gi No. 4809266
- % Identity 85.7
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- Alignment No. 17075
- gi No. 481477
- % Identity 85.7
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- Location of Alignment in SEQ ID NO 2727: from 27 to 47

- Alignment No. 17076
- gi No. 481477
- % Identity 85.7
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- Alignment No. 17077
- gi No. 481477
- % Identity 85.7
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- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 17078
- gi No. 481477
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 17079
- gi No. 481477
- % Identity 85.7
- Alignment Length 21
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- Alignment No. 17080
- gi No. 481477
- % Identity 85.7
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- Alignment No. 17081
- gi No. 485427
- % Identity 85.7
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- Alignment No. 17082
- gi No. 485518
- % Identity 85.7
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- Alignment No. 17083
- gi No. 49586
- % Identity 85.7
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- Alignment No. 17084
- gi No. 49586
- % Identity 85.7
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- Alignment No. 17085
- gi No. 49586
- % Identity 85.7
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- Location of Alignment in SEQ ID NO 2727: from 27 to 47

- Alignment No. 17086
- gi No. 510473
- % Identity 85.7
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- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 17087
- gi No. 510473
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 17088
- gi No. 510473
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 17089
- gi No. 510473
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 17090
- gi No. 510473
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 17091
- gi No. 510473
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 17092
- gi No. 510473
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 17093
- gi No. 510473
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 17094
- gi No. 510473
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 17095
- gi No. 510476
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 17096

- gi No. 5107695
- % Identity 76.2
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 17097
- gi No. 539404
- % Identity 81
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 17098
- gi No. 539935
- % Identity 85.7
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- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 17099
- gi No. 539935
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 17100
- gi No. 539935
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 17101
- gi No. 539935
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 17102
- gi No. 541546
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 17103
- gi No. 541546
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 17104
- gi No. 541546
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 17105
- gi No. 541546
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 17106
- gi No. 541546

- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 17107
- gi No. 541953
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 17108
- gi No. 541954
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 17109
- gi No. 5441519
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 17110
- gi No. 552237
- % Identity 81
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 17111
- gi No. 5523967
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 17112
- gi No. 5523969
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 17113
- gi No. 5523969
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 17114
- gi No. 5523971
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 17115
- gi No. 5523973
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 17116
- gi No. 5523975
- % Identity 85.7

- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 17117
- gi No. 5523977
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 17118
- gi No. 5523979
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 17119
- gi No. 5523979
- % Identity 72.4
- Alignment Length 29
- Location of Alignment in SEQ ID NO 2727: from 19 to 47
- Alignment No. 17120
- gi No. 5523981
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 17121
- gi No. 5523985
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 17122
- qi No. 5523987
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 17123
- gi No. 5531273
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 17124
- gi No. 5531273
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 17125
- gi No. 5531273
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 17126
- gi No. 5531273
- % Identity 85.7
- Alignment Length 21

- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 17127
- gi No. 5531273
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 17128
- gi No. 5531278
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 17129
- gi No. 5531281
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 17130
- gi No. 554564
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 17131
- gi No. 567767
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 17132
- gi No. 567767
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 17133
- gi No. 571519
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 17134
- gi No. 571519
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 17135
- gi No. 571519
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 17136
- gi No. 571519
- % Identity 81
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47

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- Alignment No. 17137
- gi No. 571519
- % Identity 85.7
- Alignment Length 21
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- Location of Alignment in SEQ ID NO 2727: from 27 to 47

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- Alignment No. 17138
- gi No. 571519
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 17139
- gi No. 576773
- % Identity 85.7
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- Location of Alignment in SEQ ID NO 2727: from 27 to 47

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- Alignment No. 17140
- gi No. 576773
- % Identity 85.7
- Alignment Length 21
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- Alignment Length 21

- Location of Alignment in SEQ ID NO 2727: from 27 to 47

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- Alignment No. 17141
- gi No. 576773
- % Identity 85.7
- Alignment Length 21
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- Location of Alignment in SEQ ID NO 2727: from 27 to 47

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- Alignment No. 17142
- gi No. 576773
- % Identity 85.7
- Alignment Length 21
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- Location of Alignment in SEQ ID NO 2727: from 27 to 47

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- Alignment No. 17143
- gi No. 576773
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
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- Alignment No. 17144

- gi No. 576775 - % Identity 85.7 - Alignment Length 21

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- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 17145
- gi No. 578545
- % Identity 77.3
- Alignment Length 22
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- Location of Alignment in SEQ ID NO 2727: from 27 to 48

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- Alignment No. 17146
- gi No. 578545
- % Identity 72.7
- Alignment Length 22
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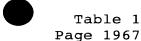
- Location of Alignment in SEQ ID NO 2727: from 27 to 48

- Alignment No. 17147
- gi No. 578546
- % Identity 81.8
- Alignment Length 22
- Location of Alignment in SEQ ID NO 2727: from 27 to 48
- Alignment No. 17148
- gi No. 578546
- % Identity 77.3
- Alignment Length 22
- Location of Alignment in SEQ ID NO 2727: from 27 to 48
- Alignment No. 17149
- gi No. 578546
- % Identity 72.7
- Alignment Length 22
- Location of Alignment in SEQ ID NO 2727: from 27 to 48
- Alignment No. 17150
- gi No. 578549
- % Identity 72.7
- Alignment Length 22
- Location of Alignment in SEQ ID NO 2727: from 27 to 48
- Alignment No. 17151
- gi No. 578549
- % Identity 72.7
- Alignment Length 22
- Location of Alignment in SEQ ID NO 2727: from 27 to 48
- Alignment No. 17152
- gi No. 578551
- % Identity 73.7
- Alignment Length 19
- Location of Alignment in SEQ ID NO 2727: from 29 to 47
- Alignment No. 17153
- gi No. 578551
- % Identity 77.3
- Alignment Length 22
- Location of Alignment in SEQ ID NO 2727: from 27 to 48
- Alignment No. 17154
- gi No. 600539
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 17155
- gi No. 602076
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 17156
- gi No. 602076
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 17157

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- gi No. 602076
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 17158
- gi No. 602076
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 17159
- gi No. 602076
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 17160
- gi No. 625174
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 17161
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- gi No. 625174
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 17162
- gi No. 625509
- % Identity 85
- Alignment Length 20
- Location of Alignment in SEQ ID NO 2727: from 27 to 46
- Alignment No. 17163
- gi No. 625509
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 17164
- gi No. 625509
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 17165
- gi No. 625509
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 17166
- gi No. 630455
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 17167
- gi No. 630479

- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 17168
- gi No. 630479
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 17169
- gi No. 630479
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 17170
- gi No. 630479
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 17171
- gi No. 630479
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 17172
- gi No. 630479
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 17173
- gi No. 70636
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 17174
- gi No. 70636
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 17175
- qi No. 70636
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 17176
- gi No. 70637
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 17177
- gi No. 70639
- % Identity 85.7



- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 17178
- gi No. 70639
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 17179
- gi No. 70639
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 17180
- gi No. 70639
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 17181
- gi No. 70640
- % Identity 81
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 17182
- gi No. 70642
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 17183
- gi No. 70642
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 17184
- gi No. 70642
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 17185
- gi No. 70642
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 17186
- gi No. 70642
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 17187
- gi No. 70643
- % Identity 85.7
- Alignment Length 21

- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 17188
- gi No. 70644
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 17189
- gi No. 70644
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 17190
- gi No. 70644
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 17191
- gi No. 70644
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 17192
- gi No. 70644
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 17193
- gi No. 70645
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 17194
- gi No. 70645
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 17195
- gi No. 70645
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 17196
- gi No. 70645
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 17197
- gi No. 70645
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47

- Alignment No. 17198 - gi No. 70646 - % Identity 85.7 - Alignment Length 21 - Location of Alignment in SEQ ID NO 2727: from 27 to 47 - Alignment No. 17199 - gi No. 70647 - % Identity 81 - Alignment Length 21 - Location of Alignment in SEQ ID NO 2727: from 27 to 47 - Alignment No. 17200 - gi No. 70647 - % Identity 81 - Alignment Length 21 - Location of Alignment in SEQ ID NO 2727: from 27 to 47 - Alignment No. 17201 - gi No. 70647 - % Identity 81 - Alignment Length 21 - Location of Alignment in SEQ ID NO 2727: from 27 to 47 - Alignment No. 17202 - gi No. 70648 - % Identity 81 - Alignment Length 21 - Location of Alignment in SEQ ID NO 2727: from 27 to 47 - Alignment No. 17203 - gi No. 70650 - % Identity 72.2 - Alignment Length 18 - Location of Alignment in SEQ ID NO 2727: from 27 to 44 - Alignment No. 17204 - gi No. 70653 - % Identity 86.4 - Alignment Length 22 - Location of Alignment in SEQ ID NO 2727: from 27 to 48 - Alignment No. 17205 - gi No. 70654 - % Identity 85.7 - Alignment Length 21 - Location of Alignment in SEQ ID NO 2727: from 27 to 47 - Alignment No. 17206
- Alignment No. 17207
- gi No. 70658

- gi No. 70657
- % Identity 85.7
- Alignment Length 21

- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47

- Location of Alignment in SEQ ID NO 2727: from 27 to 47

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- Alignment No. 17208
- gi No. 70659
- % Identity 87.5
- Alignment Length 16
- Location of Alignment in SEQ ID NO 2727: from 32 to 47
- Alignment No. 17209
- gi No. 70660
- % Identity 81.8
- Alignment Length 22
- Location of Alignment in SEQ ID NO 2727: from 27 to 48
- Alignment No. 17210
- gi No. 726391
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 17211
- gi No. 726391
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 17212
- gi No. 726391
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 17213
- gi No. 726391
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 17214
- gi No. 726391
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 17215
- gi No. 726391
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 17216
- gi No. 726391
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 17217
- gi No. 726391
- % Identity 85.7
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- Location of Alignment in SEQ ID NO 2727: from 27 to 47

- Alignment No. 17218

- Alignment Length 21

- gi No. 726391
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 17219
- gi No. 726391
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 17220
- qi No. 726391
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 17221
- gi No. 82040
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 17222
- gi No. 82040
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 17223
- gi No. 82040
- % Identity 81
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 17224
- gi No. 82040
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 17225
- gi No. 82284
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 17226
- gi No. 82287
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 17227
- gi No. 82426
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 17228
- gi No. 82426

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- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 17229
- gi No. 82512
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 17230
- gi No. 82512
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 17231
- gi No. 82733
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 17232
- gi No. 82734
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 17233
- gi No. 82734
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 17234
- gi No. 82734
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 17235
- gi No. 83594
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 17236
- gi No. 83596
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 17237
- gi No. 83596
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 17238
- gi No. 83596
- % Identity 85.7

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- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 17239
- gi No. 83596
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 17240
- gi No. 83596
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 17241
- gi No. 84151
- % Identity 86.4
- Alignment Length 22
- Location of Alignment in SEQ ID NO 2727: from 27 to 48
- Alignment No. 17242
- gi No. 84151
- % Identity 86.4
- Alignment Length 22
- Location of Alignment in SEQ ID NO 2727: from 27 to 48
- Alignment No. 17243
- gi No. 84151
- % Identity 86.4
- Alignment Length 22
- Location of Alignment in SEQ ID NO 2727: from 27 to 48
- Alignment No. 17244
- gi No. 84152
- % Identity 86.4
- Alignment Length 22
- Location of Alignment in SEQ ID NO 2727: from 27 to 48
- Alignment No. 17245
- gi No. 84152
- % Identity 86.4
- Alignment Length 22
- Location of Alignment in SEQ ID NO 2727: from 27 to 48
- Alignment No. 17246
- gi No. 84152
- % Identity 86.4
- Alignment Length 22
- Location of Alignment in SEQ ID NO 2727: from 27 to 48
- Alignment No. 17247
- gi No. 84152
- % Identity 86.4
- Alignment Length 22
- Location of Alignment in SEQ ID NO 2727: from 27 to 48
- Alignment No. 17248
- gi No. 84152
- % Identity 86.4
- Alignment Length 22

- Location of Alignment in SEQ ID NO 2727: from 27 to 48 - Alignment No. 17249 - gi No. 84337 - % Identity 83.3 - Alignment Length 18 - Location of Alignment in SEQ ID NO 2727: from 27 to 44 - Alignment No. 17250 - gi No. 84337 - % Identity 81 - Alignment Length 21 - Location of Alignment in SEQ ID NO 2727: from 27 to 47 - Alignment No. 17251 - gi No. 84478 - % Identity 85.7 - Alignment Length 21 - Location of Alignment in SEQ ID NO 2727: from 27 to 47 - Alignment No. 17252 - gi No. 84478 - % Identity 85.7 - Alignment Length 21 - Location of Alignment in SEQ ID NO 2727: from 27 to 47 - Alignment No. 17253 - gi No. 84478 - % Identity 85.7 - Alignment Length 21 - Location of Alignment in SEQ ID NO 2727: from 27 to 47 - Alignment No. 17254 - gi No. 84478
- Alignment No. 17255
- gi No. 84478
- % Identity 85.7

- % Identity 85.7 - Alignment Length 21

- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47

- Location of Alignment in SEQ ID NO 2727: from 27 to 47

- Alignment No. 17256
- gi No. 84478
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 17257
- gi No. 84478
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 17258
- gi No. 84478
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47

- Alignment Length 21

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- Alignment No. 17259
- gi No. 84478
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 17260
- gi No. 84478
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 17261
- gi No. 84478
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 17262
- gi No. 84834
- % Identity 87.5
- Alignment Length 16
- Location of Alignment in SEQ ID NO 2727: from 27 to 42
- Alignment No. 17263
- gi No. 84834
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 17264
- gi No. 84834
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 17265
- gi No. 85106
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 17266
- gi No. 85106
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 17267
- gi No. 85106
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 17268
- gi No. 870794
- % Identity 76.2
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- Location of Alignment in SEQ ID NO 2727: from 27 to 47

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- Alignment No. 17269 - gi No. 870794
- % Identity 76.2
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 17270
- gi No. 89311
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 17271
- gi No. 89311
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 17272
- gi No. 89311
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 17273
- gi No. 899115
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 17274
- gi No. 899115
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 17275
- gi No. 899608
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 17276
- gi No. 899608
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 17277
- gi No. 899608
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 17278
- gi No. 899608
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 17279

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- gi No. 899608
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 17280
- gi No. 902525
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 17281
- gi No. 902584
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 17282
- gi No. 902584
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 17283
- gi No. 902584
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 17284
- gi No. 902584
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 17285
- gi No. 902584
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 17286
- gi No. 902584
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 17287
- gi No. 902584
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 17288
- gi No. 902586
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 17289
- gi No. 902586

> - % Identity 85.7 - Alignment Length 21 - Location of Alignment in SEQ ID NO 2727: from 27 to 47 - Alignment No. 17290 - gi No. 902586 - % Identity 85.7 - Alignment Length 21 - Location of Alignment in SEQ ID NO 2727: from 27 to 47 - Alignment No. 17291 - gi No. 902586 - % Identity 85.7 - Alignment Length 21 - Location of Alignment in SEQ ID NO 2727: from 27 to 47 - Alignment No. 17292 - gi No. 902586 - % Identity 85.7 - Alignment Length 21 - Location of Alignment in SEQ ID NO 2727: from 27 to 47 - Alignment No. 17293 - gi No. 91870 - % Identity 80 - Alignment Length 20 - Location of Alignment in SEQ ID NO 2727: from 27 to 46 - Alignment No. 17294 - gi No. 91870 - % Identity 85.7 - Alignment Length 21 - Location of Alignment in SEQ ID NO 2727: from 27 to 47 - Alignment No. 17295 - gi No. 91871 - % Identity 85.7 - Alignment Length 21 - Location of Alignment in SEQ ID NO 2727: from 27 to 47 - Alignment No. 17296 - gi No. 940395 - % Identity 85.7 - Alignment Length 21 - Location of Alignment in SEQ ID NO 2727: from 27 to 47 - Alignment No. 17297 - gi No. 940395 - % Identity 85.7 - Alignment Length 21

- Location of Alignment in SEQ ID NO 2727: from 27 to 47

- Location of Alignment in SEQ ID NO 2727: from 27 to 47

- Alignment No. 17299

- Alignment No. 17298

- gi No. 940395

- gi No. 940395
- % Identity 85.7
- Alignment Length 21

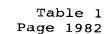
- % Identity 85.7

- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 17300
- gi No. 940395
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 17301
- gi No. 940395
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 17302
- gi No. 940395
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 17303
- gi No. 940395
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 17304
- gi No. 967985
- % Identity 88.9
- Alignment Length 18
- Location of Alignment in SEQ ID NO 2727: from 27 to 44
- Alignment No. 17305
- gi No. 99771
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 17306
- gi No. 99772
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 17307
- gi No. 99975
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- (B) Polypeptide Sequence
 - Pat. Appln. SEQ ID NO 2728
 - Ceres seq_id 1504384
 - Location of start within SEQ ID NO 2726: at 166 nt.
- - Alignment No. 17308
 - Ubiquitin family
 - Location within SEQ ID NO 2728: from 1 to 49 aa.

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(D) Related Amino Acid Sequences
   - Alignment No. 17309
   - gi No. 100490
   - % Identity 81.1
   - Alignment Length 53
   - Location of Alignment in SEQ ID NO 2728: from 1 to 49
   - Alignment No. 17310
   - gi No. 100490
   - % Identity 81.1
   - Alignment Length 53
   - Location of Alignment in SEQ ID NO 2728: from 1 to 49
   - Alignment No. 17311
   - gi No. 100490
   - % Identity 81.1
   - Alignment Length 53
   - Location of Alignment in SEQ ID NO 2728: from 1 to 49
   - Alignment No. 17312
   - gi No. 100490
   - % Identity 81.1
   - Alignment Length 53
   - Location of Alignment in SEQ ID NO 2728: from 1 to 49
   - Alignment No. 17313
   - gi No. 100524
   - % Identity 81.1
   - Alignment Length 53
   - Location of Alignment in SEQ ID NO 2728: from 1 to 49
   - Alignment No. 17314
   - gi No. 100524
   - % Identity 81.1
   - Alignment Length 53
   - Location of Alignment in SEQ ID NO 2728: from 1 to 49
   - Alignment No. 17315
   - gi No. 100524
   - % Identity 81.1
   - Alignment Length 53
   - Location of Alignment in SEQ ID NO 2728: from 1 to 49
   - Alignment No. 17316
   - gi No. 100524
   - % Identity 81.1
   - Alignment Length 53
   - Location of Alignment in SEQ ID NO 2728: from 1 to 49
   - Alignment No. 17317
   - gi No. 100524
   - % Identity 81.1
   - Alignment Length 53
   - Location of Alignment in SEQ ID NO 2728: from 1 to 49
   - Alignment No. 17318
   - gi No. 100524
   - % Identity 79.6
   - Alignment Length 54
   - Location of Alignment in SEQ ID NO 2728: from 1 to 50
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- Alignment No. 17319
- gi No. 100525
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- % Identity 81.1
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
- Alignment No. 17320
- gi No. 100525
- % Identity 81.1
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
- Alignment No. 17321
- gi No. 100525
- % Identity 81.1
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
- Alignment No. 17322
- gi No. 100525
- % Identity 81.1
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
- Alignment No. 17323
- gi No. 100598
- % Identity 78.2
- Alignment Length 55
- Location of Alignment in SEQ ID NO 2728: from 1 to 51
- Alignment No. 17324
- gi No. 100599
- % Identity 78.2
- Alignment Length 55
- Location of Alignment in SEQ ID NO 2728: from 1 to 51
- Alignment No. 17325
- gi No. 100812
- % Identity 81.1
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
- Alignment No. 17326
- gi No. 100934
- % Identity 81.1
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
- Alignment No. 17327
- gi No. 100934
- % Identity 81.1
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
- Alignment No. 17328
- gi No. 100934
- % Identity 81.1
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49



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- Alignment No. 17329
  - gi No. 100934
  - % Identity 81.1
  - Alignment Length 53
  - Location of Alignment in SEQ ID NO 2728: from 1 to 49
  - Alignment No. 17330
  - gi No. 100934
  - % Identity 81.1
  - Alignment Length 53
  - Location of Alignment in SEQ ID NO 2728: from 1 to 49
  - Alignment No. 17331
 - gi No. 100934
 - % Identity 81.1
 - Alignment Length 53
 - Location of Alignment in SEQ ID NO 2728: from 1 to 49
 - Alignment No. 17332
 - gi No. 100934
 - % Identity 81.1
 - Alignment Length 53
 - Location of Alignment in SEQ ID NO 2728: from 1 to 49
 - Alignment No. 17333
 - gi No. 100981
 - % Identity 76.7
 - Alignment Length 43
 - Location of Alignment in SEQ ID NO 2728: from 9 to 51
 - Alignment No. 17334
 - gi No. 102062
 - % Identity 77.4
 - Alignment Length 53
 - Location of Alignment in SEQ ID NO 2728: from 1 to 49
 - Alignment No. 17335
 - gi No. 102278
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
- Alignment No. 17336
- gi No. 102278
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
- Alignment No. 17337
- gi No. 102278
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
- Alignment No. 17338
- gi No. 102278
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
- Alignment No. 17339
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- gi No. 102278
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
- Alignment No. 17340
- gi No. 102278
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
- Alignment No. 17341
- gi No. 102278
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
- Alignment No. 17342
- gi No. 102279
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
- Alignment No. 17343
- gi No. 102279
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
- Alignment No. 17344
- gi No. 102279
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
- Alignment No. 17345
- gi No. 102280
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
- Alignment No. 17346
- gi No. 102280
- % Identity 77.4
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
- Alignment No. 17347
- gi No. 102280
- % Identity 79.2
- Alignment Length 53
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- Alignment No. 17348
- gi No. 102280
- % Identity 77.4
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 17349
- gi No. 102280

- % Identity 77.4
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
- Alignment No. 17350
- gi No. 102281
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
- Alignment No. 17351
- gi No. 102281
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
- Alignment No. 17352
- gi No. 102281
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
- Alignment No. 17353
- gi No. 102281
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
- Alignment No. 17354
- gi No. 102281
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
- Alignment No. 17355
- gi No. 102389
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
- Alignment No. 17356
- gi No. 103436
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
- Alignment No. 17357
- gi No. 1044940
- % Identity 76.4
- Alignment Length 55
- Location of Alignment in SEQ ID NO 2728: from 1 to 51
- Alignment No. 17358
- gi No. 104829
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
- Alignment No. 17359
- gi No. 104829
- % Identity 79.2

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- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
- Alignment No. 17360
- gi No. 104829
- % Identity 77.8
- Alignment Length 54
- Location of Alignment in SEQ ID NO 2728: from 1 to 50
- Alignment No. 17361
- gi No. 1050930
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
- Alignment No. 17362
- gi No. 10673
- % Identity 81.1
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
- Alignment No. 17363
- gi No. 1070590
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
- Alignment No. 17364
- gi No. 1070590
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
- Alignment No. 17365
- gi No. 1070590
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
- Alignment No. 17366
- gi No. 1070591
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
- Alignment No. 17367
- gi No. 1070591
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
- Alignment No. 17368
- gi No. 1070591
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
- Alignment No. 17369
- gi No. 1070591
- % Identity 79.2
- Alignment Length 53

- Location of Alignment in SEQ ID NO 2728: from 1 to 49
- Alignment No. 17370
- gi No. 1070591
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
- Alignment No. 17371
- gi No. 1070591
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
- Alignment No. 17372
- gi No. 1070591
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
- Alignment No. 17373
- gi No. 1070591
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
- Alignment No. 17374
- gi No. 1070591
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
- Alignment No. 17375
- qi No. 1076678
- % Identity 78.2
- Alignment Length 55
- Location of Alignment in SEQ ID NO 2728: from 1 to 51
- Alignment No. 17376
- gi No. 1076708
- % Identity 81.1
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
- Alignment No. 17377
- gi No. 1076708
- % Identity 81.1
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
- Alignment No. 17378
- gi No. 1076708
- % Identity 81.1
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
- Alignment No. 17379
- gi No. 1076708
- % Identity 81.1
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 17380
- gi No. 1078777
- % Identity 73.1
- Alignment Length 52
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
- Alignment No. 17381
- gi No. 1078813
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
- Alignment No. 17382
- gi No. 1078813
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
- Alignment No. 17383
- gi No. 1078813
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
- Alignment No. 17384
- gi No. 1083758
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
- Alignment No. 17385
- gi No. 1083758
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
- Alignment No. 17386
- gi No. 1083758
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
- Alignment No. 17387
- gi No. 1083758
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
- Alignment No. 17388
- gi No. 1083758
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
- Alignment No. 17389
- gi No. 1083758
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 17390
- gi No. 1083758
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
- Alignment No. 17391
- gi No. 1083758
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
- Alignment No. 17392
- gi No. 1083758
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
- Alignment No. 17393
- gi No. 1083758
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
- Alignment No. 17394
- gi No. 1101011
- % Identity 71.4
- Alignment Length 56
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
- Alignment No. 17395
- gi No. 1101011
- % Identity 71.4
- Alignment Length 56
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
- Alignment No. 17396
- gi No. 1101011
- % Identity 71.4
- Alignment Length 56
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
- Alignment No. 17397
- gi No. 1101011
- % Identity 71.4
- Alignment Length 56
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
- Alignment No. 17398
- gi No. 1101011
- % Identity 71.4
- Alignment Length 56
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
- Alignment No. 17399
- gi No. 1101011
- % Identity 71.4
- Alignment Length 56
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
- Alignment No. 17400

- gi No. 1101011 - % Identity 71.4 - Alignment Length 56 - Location of Alignment in SEQ ID NO 2728: from 1 to 49 - Alignment No. 17401 - gi No. 1101011 - % Identity 71.4 - Alignment Length 56 - Location of Alignment in SEQ ID NO 2728: from 1 to 49 - Alignment No. 17402 - gi No. 1101011 - % Identity 71.4 - Alignment Length 56 - Location of Alignment in SEQ ID NO 2728: from 1 to 49 - Alignment No. 17403 - gi No. 1101013 - % Identity 76.2 - Alignment Length 21 - Location of Alignment in SEQ ID NO 2728: from 1 to 18 - Alignment No. 17404 - gi No. 1101021 - % Identity 71.4 - Alignment Length 56 - Location of Alignment in SEQ ID NO 2728: from 1 to 49 - Alignment No. 17405 - gi No. 1101023 - % Identity 72.5 - Alignment Length 40 - Location of Alignment in SEQ ID NO 2728: from 10 to 49 - Alignment No. 17406 - gi No. 1107481 - % Identity 79.2 - Alignment Length 53 - Location of Alignment in SEQ ID NO 2728: from 1 to 49 - Alignment No. 17407 - gi No. 1107481 - % Identity 79.2 - Alignment Length 53 - Location of Alignment in SEQ ID NO 2728: from 1 to 49 - Alignment No. 17408 - gi No. 1143188 - % Identity 77.4 - Alignment Length 53 - Location of Alignment in SEQ ID NO 2728: from 1 to 49
- Alignment No. 17409 - gi No. 1143188 - % Identity 77.4

- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
- Alignment No. 17410
- gi No. 1143188

- % Identity 75.5 - Alignment Length 53 - Location of Alignment in SEQ ID NO 2728: from 1 to 49 - Alignment No. 17411 - gi No. 1167510 - % Identity 79.2 - Alignment Length 53 - Location of Alignment in SEQ ID NO 2728: from 1 to 49 - Alignment No. 17412 - gi No. 1174859 - % Identity 79.2 - Alignment Length 53 - Location of Alignment in SEQ ID NO 2728: from 1 to 49 - Alignment No. 17413 - gi No. 1174860 - % Identity 77.4 - Alignment Length 53 - Location of Alignment in SEQ ID NO 2728: from 1 to 49 - Alignment No. 17414 - gi No. 1174861 - % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
- Alignment No. 17415
- gi No. 1184755
- % Identity 76.4
- Alignment Length 55
- Location of Alignment in SEQ ID NO 2728: from 1 to 51
- Alignment No. 17416
- gi No. 1197093
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
- Alignment No. 17417
- gi No. 1197093
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
- Alignment No. 17418
- gi No. 1197093
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
- Alignment No. 17419
- gi No. 1197093
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
- Alignment No. 17420
- gi No. 1304128
- % Identity 79.2

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- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
- Alignment No. 17421
- gi No. 1304128
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
- Alignment No. 17422
- gi No. 1304128
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
- Alignment No. 17423
- gi No. 1304128
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
- Alignment No. 17424
- gi No. 1304128
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
- Alignment No. 17425
- gi No. 1304128
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
- Alignment No. 17426
- gi No. 1304128
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
- Alignment No. 17427
- gi No. 1304128
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
- Alignment No. 17428
- gi No. 1321735
- % Identity 75
- Alignment Length 40
- Location of Alignment in SEQ ID NO 2728: from 1 to 36
- Alignment No. 17429
- gi No. 1321735
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
- Alignment No. 17430
- gi No. 1326021
- % Identity 79.4
- Alignment Length 34

- Location of Alignment in SEQ ID NO 2728: from 16 to 49
- Alignment No. 17431
- gi No. 1326022
- % Identity 76.9
- Alignment Length 39
- Location of Alignment in SEQ ID NO 2728: from 11 to 49
- Alignment No. 17432
- gi No. 1326022
- % Identity 77.4
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
- Alignment No. 17433
- gi No. 1326022
- % Identity 74.1
- Alignment Length 54
- Location of Alignment in SEQ ID NO 2728: from 1 to 50
- Alignment No. 17434
- gi No. 1332579
- % Identity 81.1
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
- Alignment No. 17435
- gi No. 1332579
- % Identity 81.1
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
- Alignment No. 17436
- gi No. 1332579
- % Identity 81.1
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
- Alignment No. 17437
- gi No. 1332579
- % Identity 81.1
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
- Alignment No. 17438
- gi No. 1332579
- % Identity 81.1
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
- Alignment No. 17439
- gi No. 1332579
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
- Alignment No. 17440
- gi No. 1332579
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 17441
- gi No. 1332579
- % Identity 81.1
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
- Alignment No. 17442
- gi No. 1332579
- % Identity 81.1
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
- Alignment No. 17443
- gi No. 1332579
- % Identity 81.1
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
- Alignment No. 17444
- qi No. 1351348
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
- Alignment No. 17445
- gi No. 1351349
- % Identity 75.5
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
- Alignment No. 17446
- gi No. 1353755
- % Identity 80.6
- Alignment Length 36
- Location of Alignment in SEQ ID NO 2728: from 14 to 49
- Alignment No. 17447
- gi No. 1353755
- % Identity 77.4
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
- Alignment No. 17448
- gi No. 1353757
- % Identity 72.7
- Alignment Length 22
- Location of Alignment in SEQ ID NO 2728: from 1 to 18
- Alignment No. 17449
- gi No. 1353757
- % Identity 77.4
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
- Alignment No. 17450
- gi No. 1362008
- % Identity 81.1
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 17451gi No. 1362008% Identity 79.2Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
- Alignment No. 17452
- gi No. 1362008
- % Identity 73.6
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
- Alignment No. 17453
- gi No. 1362008
- % Identity 77.8
- Alignment Length 54
- Location of Alignment in SEQ ID NO 2728: from 1 to 50
- Alignment No. 17454
- gi No. 1362009
- % Identity 79.6
- Alignment Length 54
- Location of Alignment in SEQ ID NO 2728: from 1 to 50 $\,$
- Alignment No. 17455
- gi No. 1362010
- % Identity 83
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
- Alignment No. 17456
- gi No. 1362010
- % Identity 71.7
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
- Alignment No. 17457
- gi No. 1362010
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
- Alignment No. 17458
- gi No. 1362012
- % Identity 77.4
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
- Alignment No. 17459
- gi No. 1362012
- % Identity 77.4
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
- Alignment No. 17460
- gi No. 136665
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
- Alignment No. 17461

- gi No. 136666
- % Identity 81.1
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
- Alignment No. 17462
- gi No. 136667
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
- Alignment No. 17463
- gi No. 136668
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
- Alignment No. 17464
- gi No. 136669
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
- Alignment No. 17465
- gi No. 136670
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
- Alignment No. 17466
- gi No. 136671
- % Identity 77.4
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
- Alignment No. 17467
- gi No. 136672
- % Identity 77.4
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
- Alignment No. 17468
- gi No. 136673
- % Identity 81.1
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
- Alignment No. 17469
- gi No. 136674
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
- Alignment No. 17470
- gi No. 136675
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
- Alignment No. 17471
- gi No. 136676

- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
- Alignment No. 17472
- gi No. 136677
- % Identity 81.1
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
- Alignment No. 17473
- gi No. 136678
- % Identity 77.4
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
- Alignment No. 17474
- gi No. 1421797
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
- Alignment No. 17475
- gi No. 1480012
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
- Alignment No. 17476
- gi No. 158759
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
- Alignment No. 17477
- gi No. 158763
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
- Alignment No. 17478
- gi No. 158765
- % Identity 77.4
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
- Alignment No. 17479
- gi No. 158767
- % Identity 75.5
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
- Alignment No. 17480
- gi No. 158769
- % Identity 77.4
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
- Alignment No. 17481
- gi No. 158771
- % Identity 77.4



- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
- Alignment No. 17482
- gi No. 161281
- % Identity 77.4
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
- Alignment No. 17483
- gi No. 163575
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
- Alignment No. 17484
- gi No. 163575
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
- Alignment No. 17485
- gi No. 166336
- % Identity 77.4
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
- Alignment No. 17486
- gi No. 166336
- % Identity 77.4
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
- Alignment No. 17487
- gi No. 166336
- % Identity 77.4
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
- Alignment No. 17488
- gi No. 166336
- % Identity 77.4
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
- Alignment No. 17489
- gi No. 166336
- % Identity 77.4
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
- Alignment No. 17490
- gi No. 166336
- % Identity 77.4
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
- Alignment No. 17491
- gi No. 1666175
- % Identity 81.1
- Alignment Length 53

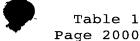


- Location of Alignment in SEQ ID NO 2728: from 1 to 49 - Alignment No. 17492 - gi No. 1675359 - % Identity 76.5 - Alignment Length 17 - Location of Alignment in SEQ ID NO 2728: from 1 to 13 - Alignment No. 17493 - gi No. 167935 - % Identity 79.2 - Alignment Length 53 - Location of Alignment in SEQ ID NO 2728: from 1 to 49 - Alignment No. 17494 - gi No. 167935 - % Identity 79.2 - Alignment Length 53 - Location of Alignment in SEQ ID NO 2728: from 1 to 49 - Alignment No. 17495 - qi No. 167935 - % Identity 77.4 - Alignment Length 53 - Location of Alignment in SEQ ID NO 2728: from 1 to 49 - Alignment No. 17496 - gi No. 167935 - % Identity 77.4 - Alignment Length 53 - Location of Alignment in SEQ ID NO 2728: from 1 to 49 - Alignment No. 17497 - gi No. 167935 - % Identity 75.9 - Alignment Length 54 - Location of Alignment in SEQ ID NO 2728: from 1 to 50
- Alignment No. 17498
- gi No. 167941
- % Identity 77.2
- Alignment Length 57
- Location of Alignment in SEQ ID NO 2728: from 1 to 53
- Alignment No. 17499
- gi No. 167945
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
- Alignment No. 17500
- gi No. 167945
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
- Alignment No. 17501
- gi No. 167945
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment Length 53

- Alignment No. 17502 - gi No. 167947 - % Identity 79.2 - Alignment Length 53 - Location of Alignment in SEQ ID NO 2728: from 1 to 49 - Alignment No. 17503 - gi No. 167947 - % Identity 79.2 - Alignment Length 53 - Location of Alignment in SEQ ID NO 2728: from 1 to 49 - Alignment No. 17504 - gi No. 167947 - % Identity 79.2 - Alignment Length 53 - Location of Alignment in SEQ ID NO 2728: from 1 to 49 - Alignment No. 17505 - gi No. 167947 - % Identity 79.2 - Alignment Length 53 - Location of Alignment in SEQ ID NO 2728: from 1 to 49 - Alignment No. 17506 - gi No. 167947 - % Identity 79.2 - Alignment Length 53 - Location of Alignment in SEQ ID NO 2728: from 1 to 49 - Alignment No. 17507 - gi No. 167947 - % Identity 79.2 - Alignment Length 53 - Location of Alignment in SEQ ID NO 2728: from 1 to 49 - Alignment No. 17508 - gi No. 167947 - % Identity 77.8 - Alignment Length 54 - Location of Alignment in SEQ ID NO 2728: from 1 to 50 - Alignment No. 17509 - gi No. 167949 - % Identity 79.2 - Alignment Length 53 - Location of Alignment in SEQ ID NO 2728: from 1 to 49 - Alignment No. 17510 - gi No. 167949 - % Identity 79.2 - Alignment Length 53 - Location of Alignment in SEQ ID NO 2728: from 1 to 49 - Alignment No. 17511 - gi No. 167949 - % Identity 79.2

- Location of Alignment in SEQ ID NO 2728: from 1 to 49



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- Alignment No. 17512
- gi No. 167949
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
- Alignment No. 17513
- gi No. 167949
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
- Alignment No. 17514
- gi No. 1684855
- % Identity 81.8
- Alignment Length 33
- Location of Alignment in SEQ ID NO 2728: from 17 to 49
- Alignment No. 17515
- gi No. 1684855
- % Identity 81.1
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
- Alignment No. 17516
- gi No. 1684855
- % Identity 81.1
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
- Alignment No. 17517
- gi No. 1684855
- % Identity 81.1
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
- Alignment No. 17518
- gi No. 1684855
- % Identity 81.1
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
- Alignment No. 17519
- gi No. 1684857
- % Identity 81.1
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
- Alignment No. 17520
- gi No. 1684857
- % Identity 81.1
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
- Alignment No. 17521
- gi No. 1684857
- % Identity 81.1
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- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 17522

- Alignment Length 53